

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 11, 2002, 22:53:37 ; Search time 78.9 Seconds
(without alignments)
484.276 Million cell updates/sec

Title: US-09-700-397-3
Perfect score: 1806
Sequence: 1 MKTIQPKMHNISWAIFTGL.....RRAGCVLLPLVLHLIKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	344	21	Human PRO337 prote
2	1806	100.0	344	21	Human protein SEQ
3	1806	100.0	344	22	Human PRO337 poly
4	1806	100.0	344	22	Amino acid sequenc
5	1806	100.0	355	22	Human polypeptide
6	1799	99.6	344	21	Human SECX Clone 1
7	1799	99.6	344	21	Human SECX Clone 1
8	1791.5	99.2	343	20	Human PRO337 prote
9	1665.5	92.2	344	22	Human polypeptide
10	1642	90.9	313	21	Human protein SEQ
11	926.5	51.3	338	17	Rat LAMP residues

12	926.5	51.3	338	17	AAW05154
13	923.5	51.1	325	17	AAW05152
14	913	50.6	361	17	AAW05172
15	908	50.3	308	17	AAW05157
16	907	50.2	315	17	AAW05158
17	905	50.1	310	17	AAW05156
18	902	49.9	304	17	AAW05155
19	886.5	49.1	287	17	AAW05159
20	885.5	49.0	287	17	AAW05160
21	852.5	47.2	326	22	AAW05167
22	823	45.6	354	22	AAW05168
23	815	45.1	352	21	AAW05167
24	796.5	44.1	252	17	AAW05167
25	795.5	44.0	252	17	AAW05168
26	720.5	39.9	281	22	AAW05168
27	603	33.4	141	22	AAW05168
28	569.5	31.5	130	22	AAW05168
29	525.5	29.1	872	22	AAW05168
30	338.5	18.7	413	22	AAW05168
31	333	18.4	315	22	AAW05168
32	306	16.9	545	22	AAW05168
33	297.5	16.5	333	22	AAW05168
34	288.5	16.0	1240	22	AAW05168
35	284.5	15.8	467	22	AAW05168
36	276	15.3	848	21	AAW05168
37	270	15.0	729	22	AAW05168
38	269	14.9	152	22	AAW05168
39	268.5	14.9	1496	20	AAW05168
40	268.5	14.9	1496	21	AAW05168
41	268.5	14.9	1498	22	AAW05168
42	267	14.8	58	21	AAW05168
43	261	14.5	1395	20	AAW05168
44	261	14.5	1395	20	AAW05168
45	260.5	14.4	496	22	AAW05168

ALIGNMENTS

RESULT 1	
AAW05154	standard; Protein; 344 AA.
ID	AAW05154
AC	AAW05154
XX	AAW05154
DT	08-FEB-2001 (first entry)
XX	08-FEB-2001 (first entry)
DE	Human PRO337 protein sequence SEQ ID NO:523.
XX	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW	expressed sequence tag; detection; cancer.
XX	Human sapiens.
OS	Human sapiens.
XX	Human sapiens.
PN	WO200053756-A2.
XX	WO200053756-A2.
PD	14-SEP-2000.
XX	14-SEP-2000.
PF	18-FEB-2000; 2000WO-US04341.
XX	18-FEB-2000; 2000WO-US04341.
XX	08-MAR-1999; 99WO-US05028.
PR	12-MAR-1999; 99US-0123957.
PR	29-MAR-1999; 99US-0126773.
PR	21-APR-1999; 99US-0130232.
PR	28-APR-1999; 99US-0131445.
PR	14-MAY-1999; 99US-0134287.
PR	23-JUN-1999; 99US-0141037.
PR	26-JUL-1999; 99US-0145698.
PR	29-OCT-1999; 99US-0162506.
PR	30-NOV-1999; 99WO-US28313.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28565.
PR	16-DEC-1999; 99WO-US30095.

Rat LAMP residues
Human LAMP residue
Rat LAMP clone 6c.
Human LAMP residue
Rat LAMP residues
Rat mature LAMP.
Human mature LAMP.
Human LAMP residue
Rat LAMP residues
Human colon cancer
Amino acid sequenc
Human PRO4993 prot
Human LAMP residue
Rat LAMP residues
Human cDNA SEQ ID
Novel human diagno
Novel human diagno
Novel human diagno
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Novel human diagno
Drosophila melanog
Human NCAM 140KD 1
Drosophila melanog
Human immunoglobul
Melanoma associate
Human p53 target m
Human peroxidase
Human secreted pro
Drosophila Robo 1
Drosophila sp. ROB
Drosophila melanog

PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78590.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
XX Claim 12; Fig 222; 636pp; English.
XX
PS AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 344 AA;
SQ

Query Match 100.0%; Score 1806; DB 21; Length 344;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLALCLFQGVPRSGDATFPKAMDNTVROGESATLRCTID 60
Db 1 mktlqpkmhnsiswailftglalclfgvprvsqdatfpkamdnvtvrgesatlrcld 60

QY 61 NRVTRVWALNRSTILYAGNDKWCIDPRVLLSNTQTOYSIFIONVDVYDEGPTCSVQTD 120
Db 61 nrvtrvawlnrstilyagndkwcldprvllsntqtqysieiqnvdydegpytcsvqtd 120

QY 121 NHPKTSRVHLIVQVSPKIVEISSDISISINEGNISLTICATGREPTVTWRHISPKAVGFV 180
Db 121 nhpktsrvhlivqvspkiveissdisinegnislticiatgreptvtwrhispkavgfv 180

QY 181 SEDEYLEIQGITREGSGDYECASANDVAAPVRRVKVTVNPPIYISEAKGTGVPVGQKGT 240
Db 181 sedeyleiqlgltregsgdyecasadvaapvrrvkvltvnyppyiseakgtgvpvgqkgt 240

QY 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 lqceasavpsaeefqwykddkrliegkgvkvenrpfslkliffnvsehdynitcvasn 300

QY 301 LGHTNASIMLFGPQAVSEVNGTSRRAGCWLPLPLVHLHLKE 344
Db 301 lghtnasimlfgpavsevsngtsrragcwlplplvhlhlk 344

RESULT 2
ID AAY57601 standard; Protein: 344 AA.
XX
XX AAY57601;
XX

DT 10-MAR-2000 (first entry)
XX
DE Human protein SEQ ID NO:1.
XX
KW Human; haematopoietic cell regulation; tissue generation; reparation;
KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmune; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease.
XX
XX Homo sapiens.
XX
PN WO9958668-A1.
XX
PD 18-NOV-1999.
XX
XX 13-MAY-1999; 99WO-JP02485.
XX
XX 14-MAY-1998; 98JP-0131815.
XX
XX (ONOV) ONO PHARM CO LTD.
XX
XX Fukushima D, Shibayama S, Tada H;
XX
XX WPI; 2000-062298/05.
DR N-PSDB; AA247892, AA247893.
XX
XX New polypeptides of human origin having cell regulatory, tissue
PT generation, coagulant and other activities -
XX
XX Claim 1; Page 38-40; 84pp; Japanese.
XX
XX The present sequence represents a specifically claimed novel human
CC protein. The novel human protein can be used in therapeutic drugs for
CC the prevention and treatment of a broad range of disorders including
CC autoimmune and infection-related immunodeficiency, inflammatory
CC disorders, and neurological diseases. The novel protein is expected of
CC having haematopoietic cell regulatory activity, tissue generation/
CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC blood coagulation and thrombus activity, and receptor/ligand activity.
XX
XX Sequence 344 AA;
SQ

Query Match 100.0%; Score 1806; DB 21; Length 344;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLALCLFQGVPRSGDATFPKAMDNTVROGESATLRCTID 60
Db 1 mktlqpkmhnsiswailftglalclfgvprvsqdatfpkamdnvtvrgesatlrcld 60

QY 61 NRVTRVWALNRSTILYAGNDKWCIDPRVLLSNTQTOYSIFIONVDVYDEGPTCSVQTD 120
Db 61 nrvtrvawlnrstilyagndkwcldprvllsntqtqysieiqnvdydegpytcsvqtd 120

QY 121 NHPKTSRVHLIVQVSPKIVEISSDISISINEGNISLTICATGREPTVTWRHISPKAVGFV 180
Db 121 nhpktsrvhlivqvspkiveissdisinegnislticiatgreptvtwrhispkavgfv 180

QY 181 SEDEYLEIQGITREGSGDYECASANDVAAPVRRVKVTVNPPIYISEAKGTGVPVGQKGT 240
Db 181 sedeyleiqlgltregsgdyecasadvaapvrrvkvltvnyppyiseakgtgvpvgqkgt 240

QY 241 LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 lqceasavpsaeefqwykddkrliegkgvkvenrpfslkliffnvsehdynitcvasn 300

QY 301 LGHTNASIMLFGPQAVSEVNGTSRRAGCWLPLPLVHLHLKE 344
Db 301 lghtnasimlfgpavsevsngtsrragcwlplplvhlhlk 344

RESULT 3

AAU12359
ID AAU12359 standard; Protein; 344 AA.
XX
AC AAU12359;
XX
DI 24-OCT-2001 (first entry)
XX
DE Human PRO337 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2001-408281/43.
DR N-PSDB; AAS21431.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
PS Claim 12; Fig 376; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.

CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 22; Length 344;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIIFTGLAALCLFQGVVVRSGDATFPKAMDNTVROGESATLRCTID 60
Db 1 mktiqpkmhnsiswaiiftglaalclfgvvpvrsgdatfpkamdnvtvrgesatlrcld 60
QY 61 NRYTRVAVLNRSTILYAGNDKWLDPVVLLSNTQTOYSIEIQNDVYDEGPYTCVQTD 120
Db 61 nrytrvavlnrstilyagndkwclpvrllsntqtqysieiqndvdydegpytcsvqtd 120
QY 121 NHPKTSRVHLIVQVSPKRIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGV 180
Db 121 nhpktsrvhlivqvspkriveissdisinegnnisltctiatgrpeptvwrhispkavgv 180
QY 181 SEDEYLEIQGTFRQSGDYECSSANDVAAPVRRVKVTNYPPIYISEAKGTGVPVGQKT 240
Db 181 sedyleiqgltfrqsgdyecssandvaapvrrvkvtnypypyiseakgtgvpvgqkgt 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 lqceasavpsaefqwkddkrliegkkgvkenrpfslkliffnvsehdynitcvasn 300
QY 301 LGHTNASIMLFGPGAVSEVSNSTSRAGCVMWLPVLVHLHLKEF 344
Db 301 lghtnasimlfgpgavsevsngtsrragcvmwlpvlvhlhlk 344

RESULT 4
AAB31204
ID AAB31204 standard; Protein; 344 AA.
XX
AC AAB31204;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO337.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
XX
PN WO200077037-A2.
XX
PD 21-DEC-2000.
XX

PF 22-MAY-2000; 2000WO-US14042.
XX
PR 15-JUN-1999; 99US-0139695.
PR 20-JUL-1999; 99US-0145070.
PR 26-JUL-1999; 99US-0145698.
PR 17-AUG-1999; 99US-0149396.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 07-DEC-1999; 99US-0169495.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrata N, Fong S, Gao W, Gerber H, Gerlitsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin JJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX WPI; 2001-050091/06.
DR N-PSDB; AAC87037.

XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -

XX
PS Claim 12; Fig 52; 244pp; English.

XX The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides; designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO348, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO187,
CC PRO327, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.

XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 22; Length 344;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMNSISWAFITGLALCLFGQVPRVRSQDATFPKAMDNVYVROGESATIRCTID 60
Db 1 mkti qpk mns is waf it gl al cl fg qv pr v rs q dat fp k am dn v y v ro ge sa ti r ct id 60
QY 61 NRYTRVWMLNSTILYAGNDKWCLDPKRVVLLNSTQTQYSIEIQNVDPYDEGPFYTCVQTD 120
Db 61 nry tr v w m l n s t i l y a g n d k w c l d p k r v v l l n s t q t q y s i e i q n v d p y d e g p f y t c v q t d 120

QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGV 180
Db 121 nh p k t s r v h l i v q v s p k i v e i s s d i s i n e g n n i s l t c i a t g r p e p t v t r h i s p k a v g v 180
QY 181 SEDEYLEIQITREQSGDYECASNDVAPVYRVKVTYVNPPIYSBAKGTGVPYQCKGT 240
Db 181 s e d e y l e i q i t r e q s g d y e c a s n d v a p v y r v k v t y v n p p i y s b a k g t g v p y q c k g t 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
Db 241 l q c e a s a v p s a e f q w k d d k r l i e g k k g k v e n r p f s l k l i f f n v s e h d y g n v t c v a s n k 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCWLPLPLVLHLILKF 344
Db 301 l g h t n a s i m l f g p g a v s e v s n g t s s r a g c w l p l p l v l h l i l k f 344

RESULT 5
AAM40499
ID AAM40499 standard; Protein; 355 AA.

XX
AC AAM40499;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 5430.

XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.

DR N-PSDB; AA159655.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

PS Example 2; SEQ ID NO 5430; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as

Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

SQ Sequence 355 AA;

Query Match	100.0%;	Score 1806;	DB 22;	Length 355;
Best local Similarity	100.0%;	Pred. No. 1e-148;		
Matches 344;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY 1 MNTIQPKMHNISWAI FTGLAALCLFQGVPVRSGDATFEPRKMDNVTYRGGESAAVLRCTID 60
|||||
Db 12 mktiqpkmhnsiswailftglaalclfqgvprsgdatlfpkrmdnvtlvrggesatlrcctid 71

QY 61 NRTRVAVLNLSTII LYAGNDKWCILDPRVVLSTNQTQYSIEIQNDVDYDEEGPYTCSVQT 120
 |||||
 Db 72 nrvtrvawlnrstllyagndkwcldprvvlslntqgysleiqndvdydespytcsvqtd 131

QY 121 NHEKTSRVHLIVQVSPKRIEISSDISEGNNISLTCIATGREPTVTWRHSPKAVGF 180
 |||||
 Db 132 mhptsrvhivqvspkrieissdisinegnislctciatgpreplvtwrnispkavgf 191

[illegible]

QY 241 LQCSASVP SAEFWYKKDKRLIEGKKGKVENRPLSKLIFENWSEHDYGNTCVASNK 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 lqcasavpsaeftwykdkrrlliegkkvgkvknrplskliffnwsehdynrytcvasnk 311

DQ 301 LGHTNASIMLFPGAVSEVSNGTSSRRACGWLPLPIVLHLKKF 344
|||||
|||
DB 312 lghtnasimlfpgavsevsngtssrragcwlplpivlhlkkf 355

RESULT	6
AAB19721	
ID	AAB19721 standard; Protein; 344 AA.

XX	
AC	AAB19721;
XX	
DT	19-FEB-2001 (first entry)

Human SECX clone 11753149.0.6-encoded protein.

SECC; human; diagnosis; therapy; cell adhesion.

Homo sapiens.

[illegible]

```
/label= signal_peptide
```

```
/label= Mature_protein
```

/note= "C-terminal membrane attachment sequence"

W0200061754-A2.

19-OCT-2000.

07-APR-2000; 2000WO-US093392.

09-APR-1999; 99US-0128514.

XX

PA (CURA-) CURAGEN CORE.
XX
PI Fernandez E, Vernet C, Shinkets R;
XX
DR WPI: 2000-679487/66.
DR N-PSDB: AAA88790.

DR N-PSDB; AAA88790.

SECX polypeptides and the nucleic acids that encode them, useful for PT

PT arthritis and immunological disorders -

PS Claim 5; Fig 2; 143pp; English.

XX The present sequence is that of the protein encoded by novel SECX
CC Clone 11753149.0.6 (see AAA88790), which resembles rat neural cell
CC adhesion molecule neurotrimin and human opioid binding protein/cell
CC adhesion molecule OBCAM. The invention provides novel SECX
CC polynucleotides (see AAA88789-804) and the secreted or
CC membrane-associated proteins encoded by them (see AAB19720-34).
CC SECX polynucleotides, polypeptides and antibodies can be used in
CC the detection, diagnosis and treatment (including gene therapy) of
CC a broad range of pathological states.

Sequence	344	AA;
----------	-----	-----

Query Match	99.6%;	Score 1799;	DB 21;	Length 344;
Best Local Similarity	99.7%;	Pred. No. 4e-148;		
Matches 343; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 MKTIQPKMHSISWALFTGLALCLFQGVPRVSGDATFPKMDNVTVRGESATLRCTID 60
|||||
Db 1 mktlqpkmhnsiswalftglalclftgvprvsgdatfpkamdntvvrsgesatlrrctid 60

QY 61 NRTYRVAWLNSTILYAGNDKWCCLDPRVLLSNTQTQYSLEIQNVVYDEEPTCTCSVQTD 120
|||||
61 nrvtrvawlnstilyagndkcldprvllsntqtqysleiqnvvdvdegpytcsvqtd 120
Db

QY 121 NHEKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGREPVTWTRHISP KAVGFV 180
|||||
|||

Db 121 nhpktsrvhlivqvspkiveissdisinegmnsltctiatgppevtwtwrnhisp kavgf v 180

```
QY      181 SEDEYLEIQGITREBQSGDYECASANDVAAPVVRVKVTIVNPPYISEAKGTGVPVGQKGT 240
      |||||
      181 sedeyleiqgitrebgsgdyecasadvaapvrivkvtvnyppyiseakgtgvpvgqkgt 240

Db
```

QY 241 LQCEASAVPSAEFQWYKDKRLIEGKKGKVENRPFSLKLPFNVS EHDYGNVTCVASNK 300
|||||
Db 241 lqceasavpsae fwykkdkrlieggkkgvkenrpfslkl ffnvs ehdynv tcvasn k 300

QY 301 LGHTNASIMLFGGAVSEVSNGTSRAGCWLPLVLHLTKF 344
 |||||
 Db 301 lqhtnasimlfgpgavsevsngtstragcwlpllvhlhllkf 344
 |||||

RESULT	7
AAB19722	
ID	AAB19722 standard; Protein; 344 AA

XX	AAB19722;
AC	
XX	
DT	19-FEB-2001 (first entry)

Human SFCX clone 11753149.0.37-encoded protein.

AA
KW
SECC: human; diagnosis; therapy; cell adhesion.

xx
xx Homo sapiens.

XX	Key	Location/Qualifiers
FH		

	x=0	/label= signal_peptide
F1	reptase	
FT		

T 3

Page 5

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FT      /label= Mature_protein
FT      Region      327..344
FT      /note= "C-terminal membrane attachment sequence"
XX      WO200061754-A2.
XX      19-OCT-2000.
XX      07-APR-2000; 2000WO-US09392.
XX      09-APR-1999; 99US-0128514.
XX      03-MAR-2000; 2000US-0128514.
XX      (CURA-) CURAGEN CORP.
XX      Fernandez E, Vernet C, Shimkets R;
XX      WPI; 2000-679487/66.
XX      N-PSDB; AAA88791.
XX      SECX polypeptides and the nucleic acids that encode them, useful for
XX      diagnosing, preventing and treating e.g. cancers, inflammation,
XX      arthritis and immunological disorders -
XX      Claim 5; Fig 3; 143pp; English.
XX      The present sequence is that of the protein encoded by novel SECX
XX      Clone 11753149.0.37 (see AAA88791), which resembles rat neural cell
XX      adhesion molecule neurotritin and human opioid binding protein/cell
XX      adhesion molecule OBCAM. The invention provides novel SECX
XX      polynucleotides (see AAA88789-804) and the secreted or
XX      membrane-associated proteins encoded by them (see AAB19720-34).
XX      SECX polynucleotides, polypeptides and antibodies can be used in
XX      the detection, diagnosis and treatment (including gene therapy) of
XX      a broad range of pathological states.
XX      Sequence 344 AA:
SQ
Query Match      99.6%; Score 1799; DB 21; Length 344;
Best Local Similarity 99.7%; Pred. No. 4e-148;
Matches 343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 MKTIQPKMHNISWATFTGLALCLFQGVPRSGDAPFPKAMDNTVVRQGESATLRCTID 60
Db      1 mkti qpkmhnsiswalfgtlaalcifgvpvrsgdatfpkamdnvtvrgesatlrctid 60
QY      61 NRVTRVAMLNKSTILYAGNDKWCIDPRVLLSNQTQYSIEIQNVYDDEGPTCSVOTD 120
Db      61 nrvtrvamlnrstilyagndkwcldprvllsntqtqysieiqnvdydegpytcsvotd 120
QY      121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNISILCIATGRPEPTVTRHISPKAVGFV 180
Db      121 nhpktsrvhlivqvspkiveissdisinegnisilciatgrpeptvtrhispkavgf 180
QY      181 SEDEYLEIQITREOSGDYECASANDYAAPVVRKVTYVNPPIYSEAKGTGVPVQOKGT 240
Db      181 sedeyleiqitreosgdycasandyaapvvrkvtyvnpypyiseakgtgvpvgokgt 240
QY      241 IQCEASAVPSAEFQWYKDKRLIEGKGVKVENRPELSKLIFFNVSEHDYGNITCVASNK 300
Db      241 iqceasavpsaefqwykdkrliegkgvkvenrpeliskliffnvsehdynitcvasn 300
QY      301 LGHTNASIMLFGPAGVSEVNGTSRRAGCWLPLPLVHLLKF 344
Db      301 lghtnasimlfgpavsevngtsrragcwlplplvhlhllkf 344
RESULT      8
AAV41773
ID      AAV41773 standard; Protein; 343 AA.
XX
AC      AAV41773;

```

```

XX      07-DEC-1999 (first entry)
DT      Human PRO337 protein sequence.
XX      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX      probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX      secreted protein; transmembrane protein.
XX      Homo sapiens.
XX      WO9946281-A2.
XX      16-SEP-1999.
XX      08-MAR-1999; 99WO-US05028.
XX      10-MAR-1998; 98US-0077450.
XX      11-MAR-1998; 98US-0077632.
XX      11-MAR-1998; 98US-0077641.
XX      11-MAR-1998; 98US-0077649.
XX      12-MAR-1998; 98US-0077791.
XX      13-MAR-1998; 98US-0078004.
XX      17-MAR-1998; 98US-0040220.
XX      20-MAR-1998; 98US-0078886.
XX      20-MAR-1998; 98US-0078910.
XX      20-MAR-1998; 98US-0078936.
XX      20-MAR-1998; 98US-0078939.
XX      25-MAR-1998; 98US-0079294.
XX      26-MAR-1998; 98US-0079656.
XX      27-MAR-1998; 98US-0079663.
XX      27-MAR-1998; 98US-0079664.
XX      27-MAR-1998; 98US-0079689.
XX      27-MAR-1998; 98US-0079728.
XX      27-MAR-1998; 98US-0079786.
XX      30-MAR-1998; 98US-0079920.
XX      30-MAR-1998; 98US-0079923.
XX      31-MAR-1998; 98US-0080105.
XX      31-MAR-1998; 98US-0080107.
XX      31-MAR-1998; 98US-0080165.
XX      31-MAR-1998; 98US-0080194.
XX      01-APR-1998; 98US-0080327.
XX      01-APR-1998; 98US-0080328.
XX      01-APR-1998; 98US-0080333.
XX      01-APR-1998; 98US-0080334.
XX      08-APR-1998; 98US-0081049.
XX      08-APR-1998; 98US-0081070.
XX      08-APR-1998; 98US-0081071.
XX      09-APR-1998; 98US-0081195.
XX      09-APR-1998; 98US-0081203.
XX      09-APR-1998; 98US-0081229.
XX      15-APR-1998; 98US-0081817.
XX      15-APR-1998; 98US-0081838.
XX      15-APR-1998; 98US-0081952.
XX      15-APR-1998; 98US-0081955.
XX      21-APR-1998; 98US-0082568.
XX      21-APR-1998; 98US-0082569.
XX      22-APR-1998; 98US-0082700.
XX      22-APR-1998; 98US-0082704.
XX      22-APR-1998; 98US-0082804.
XX      23-APR-1998; 98US-0082767.
XX      23-APR-1998; 98US-0082796.
XX      27-APR-1998; 98US-0083336.
XX      28-APR-1998; 98US-0083322.
XX      29-APR-1998; 98US-0083392.
XX      29-APR-1998; 98US-0083495.
XX      29-APR-1998; 98US-0083496.
XX      29-APR-1998; 98US-0083499.
XX      29-APR-1998; 98US-0083500.
XX      29-APR-1998; 98US-0083545.
XX      29-APR-1998; 98US-0083554.
XX      29-APR-1998; 98US-0083558.
XX      29-APR-1998; 98US-0083559.

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PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 28-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34324.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
PS Claim 12; Fig 222; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 343 AA;

Query Match 99.2%; Score 1791.5; DB 20; Length 343;
Best Local Similarity 99.7%; Pred. No. 1.8e-147;
Matches 343; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MKTIQPKMHSISWAIETGALALCLFQGVPRSGDATFPKAMDNTVYRQGESATLACTID 60
Db 1 mktiqpkmhnsiswailtjlaalcifgvprvsgdatfpkamdnvtrvgesalrlctid 60
OY 61 NRYTRVAVLNRSTILYAGNDKWCLDPRVVLISNTQTSIEIQNVVYDDEGPTCSYQTD 120
Db 61 nrytrvavlnrstilyagndkwcl DPRVVLISNTQTSIEIQNVVYDDEGPTCSYQTD 120

OY 121 NHPKTSRVHLIVQVSPKIVETSSDISINEGNNSLTCIATGRPEPTVTRHISPKAVGFV 180
Db 121 nhpktsrvhlivqvspkiveissdisinegnnsltctatgrpeptvtrhispkavgf 180
OY 181 SEDEYLEIQGITREQSGDIECSASNDVAAPVVRKVTVNVPYISKAGTGVPVGQKGT 240
Db 181 sedeyleiqgitreqsqdyecsaandvaapvrvkvtnvppyiseakgtgvpvgqkgt 240
OY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASK 300
Db 241 lqceasavpsaefqwkddkrliegkkgvkenrpfslkliffnvsehdygnvtcvask 300
OY 301 LGHTNASIMLFGPAVSEVSNSTSRAGCWLPLPLVHLLEKE 344
Db 301 lghtnasimlfgpavsevsngtsrragc-wllpllvhlhllkf 343

RESULT 9

AAM38713 AAM38713 standard; Protein; 344 AA.

AC AAM38713;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 1858.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2009; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX

DR WPI; 2001-442253/47.

DR N-PSDB; AA157869.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PT

PS Example 3; SEQ ID NO 1858; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

PF 29-MAR-1996; 96WO-US04397.
XX
PR 31-MAR-1995; 95US-0414657.
XX
PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
XX
PI Fischer I, Levitt PR, Pimenta A, Zhukareva V;
XX
DR WPI; 1996-455009/45.
DR N-PSDB; AAT42080.
XX
PT DNA encoding limbic system associated membrane protein self binding
PT domain - useful in treatment of excessive neural growth in limbic
PT system, e.g. in animal having epilepsy, Alzheimer's disease or
PT schizophrenia
XX
PS Claim 7; page 40-42; 87pp; English.

The sequences given in AAW05152-70 represent fragments of limbic system associated membrane protein (LAMP) self binding domain. LAMP is a self-binding, antibody-like cell surface adhesion protein, which causes the formation of connections between adjacent neurons. LAMP is bound by the monoclonal antibody 2G9 and is thought to be involved in the growth and differentiation of certain neurons. The protein is highly conserved and the human and rat sequences differ in only four amino acids. LAMP and the human and rat sequences can be used to treat animals with excessive neural growth in the limbic region, i.e. where the animal has epilepsy, Alzheimer's disease or schizophrenia. Neural stem cells transformed with an expression vector comprising one of these nucleic acids, can be used to treat neuropathologies involving the limbic system.

Sequence 338 AA;

Query Match	51.38; Score 926.5; DB 17; Length 338;
Best Local Similarity	55.18; Pred. No. 2.8e-72;
Matches 179; Conservative	60; Mismatches 81; Indels 5; Gaps 4
QY 20	LAALCLF-QGVPRVSRGDAFPKAMDNVTVRQGESATLRCTIDNRVTRVAMNRSTILYAG 78
Db 17	IRLLCLPLPTGLPVRSD--FNGTDNITVRGDTALLRVEDKNSKVAVINRSGILFAG 74
QY 79	NDKWCCLDPRVVLLSNTQTQYSTIEIQNVDPVDEGPRYTCVQGTDNHPKTSRVHLIVQVSPKI 138
Db 75	hdkwslpdrvelekrhaleyslrldqvdydegssytcsvgtqhepktsqyallvqvpki 134
QY 139	VEISSDISINEGNNISLFCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGTIREQSGD 198
Db 135	snissdvtvnegsnvltvcmangrpevitwrhltpigrfegeeeyleilgtiregsqk 194
QY 199	YECGASNDVAAPVVRVKVTVNPYPYISEAKGTGVPVGQKGTLOCEASAVPSAEFQWKD 258
Db 195	yeckaanevssadvkqyktvnypplitesksnealtgrgaslkceasavpabdfewyrd 254
QY 259	DKRLIEGKKGVKVENRPFSLKLFENVSEHDYGNVTCVASNKLIGHTNASIMLFGCAVSE 318
Db 255	dtr-insangleikstegqssltvntvteehygnytcvaanklgytnaslvlfrpsvrg 313
QY 319	VSNGTSRRAGCVMILPLVLHLLK 343
Db 314	i-ngsislavplwlaaslfcllisk 337
RESULT 12	
AAW05154	
ID	AAW05154 standard; Protein; 338 AA.
XX	
AC	AAW05154;
XX	
DT	22-MAY-1997 (first entry)
XX	
DE	Rat LAMP residues 1-332.

XX limbic system associated membrane protein; LAMP; self binding domain;
 KW antibody-like; cell surface adhesion protein; neuron;
 KW monoclonal antibody; 2G9; growth; differentiation; epilepsy;
 KW Alzheimer's disease; schizophrenia; neural stem cell.
 XX
 OS *Rattus rattus*.
 XX

FH	key	location/qualifiers
FT	Peptide	1..28
FT		/note= "Signal peptide"
FT	Protein	29...338
FT		/note= "Mature protein"

PN W09630052-A1.

PD 03-OCT-1996.

PF 29-MAR-1996; 96WO-US04397.

PR 31-MAR-1995; 95US-0414657-

PA (UMDJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.

PI Fischer I, Levitt PR, Pimenta A, Zhukareva V,

DR WPI; 1996-455009/45.

DR N-PSDB; AAT42081.

PT DNA encoding limbic system associated membrane protein cell binding

system, e.g. in animal having epilepsy, Alzheimer's disease or

PT schizophrēnia

PS Claim 4; Page 43-45; 87pp; English.

xx The sequences given in AAM05152-70 represent fragments of limbic system associated membrane protein (LAMP) self binding domain. LAMP is a self-binding, antibody-like cell surface adhesion protein, which causes the formation of connections between adjacent neurons. LAMP is bound by the monoclonal antibody 2G9 and is thought to be involved in the growth and differentiation of certain neurons. The protein is highly conserved and the human and rat sequences differ in only four amino acids. LAMP nucleic acids, or soluble LAMP analogues, can be used to treat an animal with excessive neural growth in the limbic region, i.e. where the animal has epilepsy, Alzheimer's disease or schizophrenia. Neural stem cells transformed with an expression vector comprising one of these nucleic acids, can be used to treat neuropathologies involving the limbic system.

SQ	Sequence	338	AA;
----	----------	-----	-----

Query Match	51.3%;	Score 926.5;	DB 17;	Length 338;
Best Local Similarity	55.1%;	Pred. No. 2.8e-72;		
Matches 179;	Conservative	60;	Mismatches 81;	Indels 5;
				Gaps 4

```

OY      20 LAALCLF-QGVPRSGDATEPKAMDNVTRQGESATLRCTIDNRYRVAWLNSTILYAG 78
        |  |||  |::|||  |  :  ::|||::|  |||  ::|  ::|||  |::||
Db      17 lrlcllptglprsvd--fgrtdnclvrgdta:lrcvcdkmskvawlnrsgllfag 74

```

79 NDKWCLDPVLLSNTQTQYSIEIQNVVYDEGPTYCSVQTDNHPKTSRVHLIVQVSPKI 138

Db 75 hdkwsl dprvelekrhaleyslr iqkvdydegsvtcsvqtqhep ktsqvyllvqvppk1 134

139 VEISSDISINEGNNISLTCTATGRPEPTVTWRHISPKAVGVSEDEYLEIQGITREQSGD 198

Db 135 snissdvtnegsnvtlvcmangrpepvtwrhltplogrefegeeeyleilgltreqsyk 194

199 YEC SASNDVAAPVVRVKVTVNPYISEAKGTGVPVGQKGTLCCEASAVPSAEHQWKD 250

Db 195 yeckanevssadvkvktvnpptitesksneattgrqaslkceasavpappdewyrd 234

CC differentiation of certain neurons. The protein is highly conserved
CC and the human and rat sequences differ in only four amino acids. LAMP
CC nucleic acids, or soluble LAMP analogues, can be used to treat an animal
CC with excessive neural growth in the limbic region, i.e where the animal
CC has epilepsy, Alzheimer's disease or schizophrenia. Neural stem cells
CC transformed with an expression vector comprising one of these nucleic
CC acids, can be used to treat neuropathologies involving the limbic
CC system.
XX
SQ Sequence 361 AA;

Query Match 50.6%; Score 913; DB 17; Length 361;
Best Local Similarity 51.7%; Pred. No. 4.5e-71;
Matches 180; Conservative 60; Mismatches 80; Indels 28; Gaps 5;

QY 20 LAALCLF-QGVPVRSGDATFPKAMDNTVRQGESATLRCTIDNRYTRVAMLNSTILYAG 78
Db 17 lrlcllptglpvrsvd--fnrgtdnltrvgdtaillrcvledknskvwalnrsqllfag 74
QY 79 NDKWCIDPRVLLSNQTQYSIEIQNDVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 hdkwsldprvelekrhaleyslrlqkdvdydegsvtqthepktsqyylivqvpki 134
QY 139 VEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
Db 135 snissdvtvnegsnvlvcmangrpepvtlwrhlptlgrfegeeeyleilgtreqsgx 194
QY 199 YECASANDVAAPVRRVKVTNPPYISAKGTGVPVGQKGTIQCEASAVPSAEFQWYKD 258
Db 195 yeckanevssadvkqvkvtvnyppitltesksneattgrqaslkceasavpdpfewrd 254
QY 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLF----- 311
Db 255 dtr-insangleikstegqslvtvnteelhygnytcvaanklgytnaslvlfrkrlptv 313
QY 312 -----GPGAVSEVSNGTSSRAGCVWLLPLVLVHLLK 343
Db 314 phpiqelgtlvhfkqkqpgsvrgl-ngsislavplwllaaslfcljlsk 360

RESULT 15
AAM05157
ID AAM05157 standard; Protein; 308 AA.
XX
AC AAM05157;
XX
DT 22-MAY-1997 (first entry)
XX
DE Human LAMP residues 8-315.
XX
KW limbic system associated membrane protein; LAMP; self binding domain;
KW antibody-like; cell surface adhesion protein; neuron;
KW monoclonal antibody; 269; growth; differentiation; epilepsy;
KW Alzheimer's disease; schizophrenia; neural stem cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "Represents residues 8-28 of signal peptide"
FT Protein 22..308
FT Protein /note= "Represents residues 29-315 of mature protein"
XX
PN WO9630052-A1.
XX
PD 03-OCT-1996.
XX
PF 29-MAR-1996; 96WO-US04397.
XX
PR 31-MAR-1995; 95US-0414657.
XX
PA (UMDU-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.

XX
PI Fischer I, Levitt PR, Pimenta A, Zhukareva V;
XX
DR WPI; 1996-455009/45.
DR N-PSDB; AAT42084.
XX

PT DNA encoding limbic system associated membrane protein self binding
PT domain - useful in treatment of excessive neural growth in limbic
PT system, e.g. in animal having epilepsy, Alzheimer's disease or
PT schizophrenia
XX

PS Claim 4; Page 50-52; 87pp; English.

XX
CC The sequences given in AAM05152-70 represent fragments of limbic system
CC associated membrane protein (LAMP) self binding domain. LAMP is a
CC self-binding, antibody-like cell surface adhesion protein, which causes
CC the formation of connections between adjacent neurons. LAMP is bound by
CC the monoclonal antibody 269 and is thought to be involved in the growth
CC and differentiation of certain neurons. The protein is highly conserved
CC and the human and rat sequences differ in only four amino acids. LAMP
CC nucleic acids, or soluble LAMP analogues, can be used to treat an
CC animal with excessive neural growth in the limbic region, i.e where
CC the animal has epilepsy, Alzheimer's disease or schizophrenia. Neural
CC stem cells transformed with an expression vector comprising one of
CC these nucleic acids, can be used to treat neuropathologies involving
CC the limbic system.
XX

SQ Sequence 308 AA;

Query Match 50.3%; Score 908; DB 17; Length 308;
Best Local Similarity 56.3%; Pred. No. 9.9e-71;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

QY 20 LAALCLF-QGVPVRSGDATFPKAMDNTVRQGESATLRCTIDNRYTRVAMLNSTILYAG 78
Db 10 lrlcllptglpvrsvd--fnrgtdnltrvgdtaillrcvledknskvwalnrsqllfag 67
QY 79 NDKWCIDPRVLLSNQTQYSIEIQNDVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 hdkwsldprvelekrhaleyslrlqkdvdydegsvtqthepktsqyylivqvpki 127
QY 139 VEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
Db 128 snissdvtvnegsnvlvcmangrpepvtlwrhlptlgrfegeeeyleilgtreqsgk 187
QY 199 YECASANDVAAPVRRVKVTNPPYISAKGTGVPVGQKGTIQCEASAVPSAEFQWYKD 258
Db 188 yeckanevssadvkqvkvtvnyppitltesksneattgrqaslkceasavpdpfewrd 247
QY 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFPGAVSE 318
Db 248 dtr-insangleikstegqslvtvnteelhygnytcvaanklgytnaslvlfrpgsvrg 306
QY 319 VS 320
Db 307 in 308

Search completed: July 12, 2002, 00:33:37
Job time: 6000 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 20:32:12 ; Search time 435.78 Seconds

(without alignments)
4065.941 Million cell updates/sec

Title: US-09-700-397-1

Perfect score: 1032

Sequence: 1 atgaacaacatccagccaaa.....tgcacctgctctcaattt 1032

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

- N_Geneseq_032802:*
- 1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
 - 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
 - 3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
 - 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
 - 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
 - 6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
 - 7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
 - 8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
 - 9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
 - 10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
 - 11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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 - 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
 - 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
 - 15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
 - 16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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 - 18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
 - 19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
 - 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
 - 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
 - 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
 - 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
 - 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	1032	21	AAZ47892 Human protein enco
2	1032	100.0	1679	20	AAZ34324 Human PRO337 nucle
3	1032	100.0	1679	21	AAC78590 Human PRO337 nucle
4	1032	100.0	1679	22	AAS21431 Human cDNA sequenc
5	1032	100.0	1679	22	AAC87037 Nucleotide sequenc
6	1032	100.0	1693	21	AAZ47893 Human protein enco
7	1030.4	99.8	1603	21	AAA88790 Human SECX CDNA C1
8	1030.4	99.8	2012	21	AAA88791 Human SECX CDNA C1
9	998	96.7	1690	22	AA159655 Human polynucleoti

10	952	92.2	1678	22	AA157869	Human polynucleoti
11	939	91.0	939	21	AAZ47894	Human protein enco
12	670.8	65.0	832	21	AAA44536	Human secreted exp
13	536	51.9	3069	14	AAO51015	Rat opioid recepto
14	518.2	50.2	2179	14	AAO51017	Rat opioid recepto
15	518.2	50.2	2337	14	AAO51016	Rat opioid recepto
16	492	47.7	503	20	AAZ34325	Human EST DNA42301
17	492	47.7	503	21	AAZ34325	Human EST DNA42301
18	362.2	35.1	537	22	AAC91321	Human polynucleoti
19	352.4	34.1	484	23	AAZ78035	DNA encoding novel
20	340.6	33.0	924	17	AAZ42084	Human LAMP residue
21	340.6	33.0	977	17	AAZ42079	Human LAMP residue
22	340.6	33.0	1014	17	AAZ42081	Human LAMP residue
23	340.6	33.0	1238	17	AAZ42080	Rat LAMP coding se
24	338.6	32.8	861	17	AAZ42082	Human LAMP residue
25	338.6	32.8	912	17	AAZ42085	Human mature LAMP
26	337.4	32.7	945	17	AAZ42085	Rat LAMP residues
27	337	32.7	930	17	AAZ42083	Rat mature LAMP co
28	333.8	32.3	861	17	AAZ42087	Rat LAMP residues
29	331.8	32.2	1307	17	AAZ42116	Rat LAMP clone 6c
30	330	32.0	452	22	AAZ93346	Spinal cord tissue
31	325.2	31.5	1153	22	AAH34425	Human colon cancer
32	316.2	30.6	333	21	AAZ19214	Human secreted pro
33	303.6	29.4	756	17	AAZ42094	Human LAMP residue
34	298.2	28.9	756	17	AAZ42095	Rat LAMP residues
35	292.4	28.3	443	23	AAZ78034	DNA encoding novel
36	272.6	26.4	4834	22	AAZ87055	Nucleotide sequenc
37	269.4	26.1	2840	21	AAZ78596	Human PRO493 nucl
38	240.8	23.3	2813	22	ABA06475	Human cDNA SEQ ID
39	220.6	21.4	4656	22	AAZ28811	Human immunoglobul
40	217.8	21.1	2883	23	AAZ78003	DNA encoding novel
41	193.6	18.8	352	21	AAZ02777	Human secreted pro
42	163.2	15.8	585	22	AAZ93597	Umbilical vein end
43	103.8	10.1	767	23	AAZ78037	DNA encoding novel
44	100	9.7	219	17	AAZ42088	Human LAMP residue
45	99	9.6	693	23	AAZ78038	DNA encoding novel

ALIGNMENTS

RESULT 1
AAZ47892
ID AAZ47892 standard; cDNA; 1032 BP.

XX AAZ47892;

DT 10-MAR-2000 (first entry)

DE Human protein encoding cDNA SEQ ID NO:2.

KW Human; haematopoietic cell regulation; tissue generation; reparation;
KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmune; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1032

FT /tag= a

PN W09958668-A1.

PD 18-NOV-1999.

PF 13-MAY-1999; 99WO-JP02485.

PR 14-MAY-1998; 98JP-0131815.

PA (ONOV) ONO PHARM CO LTD.

PI Fukushima D, Shibayama S, Tada H;
XX WPI; 2000-062298/05.
DR P-PSDB; AAY57601.
XX
PT New polypeptides of human origin having cell regulatory, tissue
PT generation, coagulant and other activities -
XX
PS Claim 4; Page 41; 84pp; Japanese.

CC The present sequence encodes a specifically claimed novel human protein.
CC The novel human protein can be used in therapeutic drugs for the
CC prevention and treatment of a broad range of disorders including
CC autoimmune and infection-related immunodeficiency, inflammatory
CC disorders, and neurological diseases. The novel protein is expected of
CC having haematopoietic cell regulatory activity, tissue generation/
CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC blood coagulation and thrombus activity, and receptor/ligand activity.

XX Sequence 1032 BP; 267 A; 281 C; 270 G; 214 T; 0 other;

Query Match 100.0%; Score 1032; DB 21; Length 1032;
Best Local Similarity 100.0%; Pred. No. 6.1e-310;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaccatccagccaaaatgcaaatctctcttggcaatcttcaagggtc 60
Db 1 atgaaccatccagccaaaatgcaaatctctcttggcaatcttcaagggtc 60
QY 61 gctgctctgtctcttccaaagggtgcccgtgcgcagcgagatgcccacttcccaaa 120
Db 61 gctgctctgtctcttccaaagggtgcccgtgcgcagcgagatgcccacttcccaaa 120
QY 121 gctatggacaacgtgacggtcccgaggggagagcgccacctcaagtcaattatgac 180
Db 121 gctatggacaacgtgacggtcccgaggggagagcgccacctcaagtcaattatgac 180
QY 181 aaccgggtcaccgggtgtgctgtctaaaccgcagcaccatctctatgtctggaatgac 240
Db 181 aaccgggtcaccgggtgtgctgtctaaaccgcagcaccatctctatgtctggaatgac 240
QY 241 aagtgtgctgtgacccctcgcggtgtccttctgagcaaccaccaagcagctacagcacc 300
Db 241 aagtgtgctgtgacccctcgcggtgtccttctgagcaaccaccaagcagctacagcacc 300
QY 301 gagatccagaacgtgagtgatgacgagggcccttacacctgtctggtgcagacagac 360
Db 301 gagatccagaacgtgagtgatgacgagggcccttacacctgtctggtgcagacagac 360
QY 361 aaccaccccaagaaccttaggtgtccacctatgtgcaagtatctcccaaatgttagag 420
Db 361 aaccaccccaagaaccttaggtgtccacctatgtgcaagtatctcccaaatgttagag 420
QY 421 attcttcagatatctccatnaatgaagggaacaatatagcctcacctgcatagcaact 480
Db 421 attcttcagatatctccatnaatgaagggaacaatatagcctcacctgcatagcaact 480
QY 481 ggtagaccagagcctacggttacttggagacacatctctccaaagcgttggcttgtg 540
Db 481 ggtagaccagagcctacggttacttggagacacatctctccaaagcgttggcttgtg 540
QY 541 agtgaagacgaataacttggaaattcagggcatacccggtgagcagtcagggtactagag 600
Db 541 agtgaagacgaataacttggaaattcagggcatacccggtgagcagtcagggtactagag 600
QY 601 tgcagtgctccaatgacgtgcccgtgtgtacgagagtaaaagtcaccgtgaac 660
Db 601 tgcagtgctccaatgacgtgcccgtgtgtacgagagtaaaagtcaccgtgaac 660
QY 661 tatccaccatacatctcagaagccaaggttacaggtgtcccggtgggacaaagggtgaca 720
Db 661 tatccaccatacatctcagaagccaaggttacaggtgtcccggtgggacaaagggtgaca 720

QY 721 ctgcagtgtaagcctcagcagctccctcagcagaattccagtggtacaaagatgacaaa 780
Db 721 ctgcagtgtaagcctcagcagctccctcagcagaattccagtggtacaaagatgacaaa 780
QY 781 agactgattgaagaaagaaggggtgaaagtggaaaaacagaccttctctcaaaactc 840
Db 781 agactgattgaagaaagaaggggtgaaagtggaaaaacagaccttctctcaaaactc 840
QY 841 atctcttcaatgtctctgaacatgactatggaaactacacttgcgtgctcccaacaag 900
Db 841 atctcttcaatgtctctgaacatgactatggaaactacacttgcgtgctcccaacaag 900
QY 901 ctgggcacacccaatgccaagcatcatgtattgttccaggcgccgtcagcaggtgagc 960
Db 901 ctgggcacacccaatgccaagcatcatgtattgttccaggcgccgtcagcaggtgagc 960
QY 961 aacggcacgtcgagggagggcaggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Db 961 aacggcacgtcgagggagggcaggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
QY 1021 ctctccaattt 1032
Db 1021 ctctccaattt 1032

RESULT 2

AAZ34324
ID AAZ34324 standard; cDNA; 1679 BP.

XX AAZ34324;

DT 07-DEC-1999 (first entry)

XX Human PRO337 nucleotide sequence.

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.

OS Homo sapiens.

XX W09946281-A2.

PD 16-SEP-1999.

PF 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.

PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR P-PSDB; AAY41773.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PI useful for treating blood coagulation disorders, cancers and cellular

PT adhesion disorders -
XX
PS Claim 2; Fig 221; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
XX invention.
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1032; DB 20; Length 1679;
Best Local Similarity 100.0%; Pred. No. 8e-310;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaacatccagccaaaaatgacaaatctctctcttcttggcaatctcaagggctg 60
Db 134 atgaaaacatccagccaaaaatgacaaatctctctcttcttggcaatctcaagggctg 193
QY 61 gctgtctgtgtctctccaaagagtgcccggtgcgcagcgagatgcccacttcccaaa 120
Db 194 gctgtctgtgtctctccaaagagtgcccggtgcgcagcgagatgcccacttcccaaa 253
QY 121 gctatgacaacgtgacggtcccgccagggagagcgccaccctcagtgacattatgac 180
Db 254 gctatgacaacgtgacggtcccgccagggagagcgccaccctcagtgacattatgac 313
QY 181 aaccgggtcaccgggtgctgtgtctaaaccgcagcacatcctctatctggaatgac 240
Db 314 aaccgggtcaccgggtgctgtgtctaaaccgcagcacatcctctatctggaatgac 373
QY 241 aagtgtgtccttgatctcgcgtgtgtctcttgagcaacacccaagcagtlacagcgc 300
Db 374 aagtgtgtccttgatctcgcgtgtgtctcttgagcaacacccaagcagtlacagcgc 433
QY 301 gagatccagaacgtgagtgtatagcagagggcccttacacctgtcgtgcagacagac 360
Db 434 gagatccagaacgtgagtgtatagcagagggcccttacacctgtcgtgcagacagac 493
QY 361 aaccacccaagaaccttaggtgccacctatgtgcaggtatctcccaaatgttagag 420
Db 494 aaccacccaagaaccttaggtgccacctatgtgcaggtatctcccaaatgttagag 553
QY 421 attcttcagatatctccatgaatgaagggaacaatatatagcctcaccctgcatagcaact 480
Db 554 attcttcagatatctccatgaatgaagggaacaatatatagcctcaccctgcatagcaact 613
QY 481 ggtagaccagacctacggttaacttggagacacatctctcccaagcggttggttgg 540
Db 614 ggtagaccagacctacggttaacttggagacacatctctcccaagcggttggttgg 673
QY 541 agtgaagacgaatacttggaaattcagggcatacccgaggagcagtgaggagactagag 600
Db 674 agtgaagacgaatacttggaaattcagggcatacccgaggagcagtgaggagactagag 733
QY 601 tgcagtgctcccaatgacgtgcccgcgcgctgtgtaagagatgaaggtcacccgtgaac 660
Db 734 tgcagtgctcccaatgacgtgcccgcgcgctgtgtaagagatgaaggtcacccgtgaac 793
QY 661 taccacacatatttcagaagccaagggtacaggtgtcccccgttgagcaaaagggagaca 720
Db 794 taccacacatatttcagaagccaagggtacaggtgtcccccgttgagcaaaagggagaca 853
QY 721 ctgcaggtgtgaagcctcagcagctccctcagcagaatctccagtggtacaaggtagaca 780
Db 853 ctgcaggtgtgaagcctcagcagctccctcagcagaatctccagtggtacaaggtagaca 921

Db 854 ctgcagtgtagcctcagcagtcctccctcagcagaattcccaagtgtacaagatgacaaa 913
QY 781 agactgattgaagaaagaagggtgaaattgaaacacacaccttctctcctcaaac 840
Db 914 agactgattgaagaaagaagggtgaaattgaaacacacaccttctctcctcaaac 973
QY 841 atctctcctcaatgtctctgaacatgactatgggaactacacttgcgtgacctccaaac 900
Db 974 atctctcctcaatgtctctgaacatgactatgggaactacacttgcgtgacctccaaac 1033
QY 901 ctgggccacacccaatgccaacatcatgtattgtccaggcgccgcaagcgagtgagc 960
Db 1034 ctgggccacacccaatgccaacatcatgtattgtccaggcgccgcaagcgagtgagc 1093
QY 961 aacggcacgtcaggaagggcaggtcgtctgtgctgtgacctctctgtgcttgcacctg 1020
Db 1094 aacggcacgtcaggaagggcaggtcgtctgtgctgtgacctctctgtgcttgcacctg 1153
QY 1021 ctctcctcaattt 1032
Db 1154 ctctcctcaattt 1165

RESULT 3
AAC78590
ID AAC78590 standard; cDNA; 1679 BP.

XX AAC78590;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO337 nucleotide sequence SEQ ID NO:522.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
XX
DR WPI: 2000-611443/58.
DR P-PSDB; AABA44329.

XX Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 2; Fig 221; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1032; DB 21; Length 1679;
Best Local Similarity 100.0%; Pred. No. 8e-310;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaaatgccaattctatctcttggcaatcttcaggggctg 60
Db 134 atgaaaaccatccagccaaaatgccaattctatctcttggcaatcttcaggggctg 193
QY 61 gctgctctgtctctctcctcgaaggaagtgccgtgctgcagcgagatgccaacttcccaaa 120
Db 194 gctgctctgtctctctcctcgaaggaagtgccgtgctgcagcgagatgccaacttcccaaa 253
QY 121 gctatgacaacgtgacggtccgcagggggagagcgccaccctcaggtgcaatttgac 180
Db 254 gctatgacaacgtgacggtccgcagggggagagcgccaccctcaggtgcaatttgac 313
QY 181 aaccgggtcaccgggtggtgctgtcctaaccgcagcaccatctctatgtggaatgac 240
Db 314 aaccgggtcaccgggtggtgctgtcctaaccgcagcaccatctctatgtggaatgac 373
QY 241 aagtgtgctgtgacatctcgtcgtgtctctctgagcaaacccaaacgagtaacgac 300
Db 374 aagtgtgctgtgacatctcgtcgtgtctctctgagcaaacccaaacgagtaacgac 433
QY 301 gagatccagaacgtgagatgtgtatgacgagggcccttacacctgtcgtgacagacac 360
Db 434 gagatccagaacgtgagatgtgtatgacgagggcccttacacctgtcgtgacagacac 493
QY 361 aaccacccaaagacctctaggtgtccacctcatgtgtcaagtatctccaaatgtagag 420
Db 494 aaccacccaaagacctctaggtgtccacctcatgtgtcaagtatctccaaatgtagag 553
QY 421 attcttcagatatctccattatgaaggaacaaatatattagcttcacctgcatagaact 480
Db 554 attcttcagatatctccattatgaaggaacaaatatattagcttcacctgcatagaact 613
QY 481 gtagaccagagcctacgttacttggagacacatctctccaaagcggttgcttg 540
Db 614 gtagaccagagcctacgttacttggagacacatctctccaaagcggttgcttg 673
QY 541 agtgaagacgaatacttgaataatcagggcatcaccgggagtcagtgagtaagag 600
Db 674 agtgaagacgaatacttgaataatcagggcatcaccgggagtcagtgagtaagag 733
QY 601 tgcagtgctcccaatgacgtggtggtggtgagagtaaggttaacggtgaac 660
Db 734 tgcagtgctcccaatgacgtggtggtggtgagagtaaggttaacggtgaac 793
QY 661 tatccacatacatctcagaagcgaaggtacaggtgtcccggtgagcaaaaggggaca 720
Db 794 tatccacatacatctcagaagcgaaggtacaggtgtcccggtgagcaaaaggggaca 853

QY 721 ctgcagtgtgaagcctcagcagctccctcagcagaattccagtgtgtacaagatgacaaa 780
|||||
Db 854 ctgcagtgtgaagcctcagcagctccctcagcagaattccagtgtgtacaagatgacaaa 913
QY 781 agactgtatgaagaaaggggtgaaagtgtgaaacagaccttctctcaaaatc 840
|||||
Db 914 agactgtatgaagaaaggggtgaaagtgtgaaacagaccttctctcaaaatc 973
QY 841 atctcttcaatgtctctgaacatgactatggaactacacttgcgtggtccccaacag 900
|||||
Db 974 atctcttcaatgtctctgaacatgactatggaactacacttgcgtggtccccaacag 1033
QY 901 ctgggccacacccaatgcccagcatcatgtattgttccaggcgcgtcagcgaggtgagc 960
|||||
Db 1034 ctgggccacacccaatgcccagcatcatgtattgttccaggcgcgtcagcgaggtgagc 1093
QY 961 aacggcagctcgagagggcgagcgtcgtctgtcgtcctcttctgtcttgacactg 1020
|||||
Db 1094 aacggcagctcgagagggcgagcgtcgtcgtcgtcctcttctgtcttgacactg 1153
QY 1021 ctcttcaattt 1032
Db 1154 ctcttcaattt 1165

RESULT 4

AAS21431
ID AAS21431 standard; cDNA; 1679 BP.

AC AAS21431;

DT 24-OCT-2001 (first entry)

DE Human cDNA sequence encoding for PRO337 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.

OS Homo sapiens.

PN WO200140466-A2.

PD 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12359.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
PS Claim 3; Fig 375; 813pp; English.

CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1032; DB 22; Length 1679;
Best Local Similarity 100.0%; Pred. No. 8e-310;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaanaatgacaattctatctcttgggaactcttcaggggctg 60
|||||
Db 134 atgaaaccatccagccaanaatgacaattctatctcttgggaactcttcaggggctg 193
QY 61 gctgtctgtgtctcttccaagagtgcccggtgcgacgagatgccacttcccaaa 120
|||||
Db 194 gctgtctgtgtctcttccaagagtgcccggtgcgacgagatgccacttcccaaa 253
QY 121 gctatggacaacgtgacggtccggcaggggagagcgccaccctcagtgtgcaattgac 180
|||||
Db 254 gctatggacaacgtgacggtccggcaggggagagcgccaccctcagtgtgcaattgac 313
QY 181 aaccgggtcacccgggtgtgctgtgtaaacgcagcaccatctctatgttggaaatgac 240
|||||
Db 314 aaccgggtcacccgggtgtgctgtgtaaacgcagcaccatctctatgttggaaatgac 373
QY 241 aagtgtgctgtgacatcctcggtgtgtcctcttgagcaacaccccaacagcagtaacatc 300
|||||
Db 374 aagtgtgctgtgacatcctcggtgtgtcctcttgagcaacaccccaacagcagtaacatc 433
QY 301 gagatccagaacgtgtgatgtatgacgagggcccttacacctgtcgtgtgacagacagac 360
|||||
Db 434 gagatccagaacgtgtgatgtatgacgagggcccttacacctgtcgtgtgacagacagac 493
QY 361 aaccacccaagaacctaggggtccacctcatgtgtgcaaglatctccaaaattgtagag 420

Db 134 atgaaaccatccagccaaaatgacaaattctatctcttgaggcaatcttcacgggctg 193
QY 61 gctgctctgtgtctcttccaaaggagtgcccgctgacgagcgagatgcaccttcccaaa 120
Db 194 gctgctctgtgtctcttccaaaggagtgcccgctgacgagcgagatgcaccttcccaaa 253
QY 121 gctatggacaacgtgacggtccggacgggggagagcgccacccctcaggtgcactattgac 180
Db 254 gctatggacaacgtgacggtccggacgggggagagcgccacccctcaggtgcactattgac 313
QY 181 aaccgggtacacccgggtgctgctgctaaacccgacacccatcctctatgctggaatgac 240
Db 314 aaccgggtacacccgggtgctgctgctaaacccgacacccatcctctatgctggaatgac 373
QY 241 aagtggtgctggtatccctcgctgctgctcttgagcaaccccaacgagtagacatc 300
Db 374 aagtggtgctggtatccctcgctgctgctcttgagcaaccccaacgagtagacatc 433
QY 301 gagatccagaacgtggtatgtatgacgagggcccttaacacctgctgctgacagac 360
Db 434 gagatccagaacgtggtatgtatgacgagggcccttaacacctgctgctgacagac 493
QY 361 aaccacccaaagacccctcagggtccacccatctgtgcaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagacccctcagggtccacccatctgtgcaagtatctcccaaatgttagag 553
QY 421 attctctcagatatctcctaatatgaaagggaacaaatatagccctcactgacatagcaact 480
Db 554 attctctcagatatctcctaatatgaaagggaacaaatatagccctcactgacatagcaact 613
QY 481 ggtagaccagagcctcaggttactcttgagagacacatctctcccaaacggttgcttgtg 540
Db 614 ggtagaccagagcctcaggttactcttgagagacacatctctcccaaacggttgcttgtg 673
QY 541 agtgaagacgaatactctggaatactcagggacacaccccgagagcagtcagggagactagag 600
Db 674 agtgaagacgaatactctggaatactcagggacacaccccgagagcagtcagggagactagag 733
QY 601 tgcagtgctccaatgacgtgacggtgacggcccgctgtgacgagagaaaggtcacogtgaac 660
Db 734 tgcagtgctccaatgacgtgacggtgacggcccgctgtgacgagagaaaggtcacogtgaac 793
QY 661 tatccaccatacatctcagaagccaagggtacaggtgtcccggtgggacaaaaggggaca 720
Db 794 tatccaccatacatctcagaagccaagggtacaggtgtcccggtgggacaaaaggggaca 853
QY 721 ctgcagtgtagagcctcagcagtcctccctcagcagagaattccagtggtacaaagtgacaaa 780
Db 854 ctgcagtgtagagcctcagcagtcctccctcagcagagaattccagtggtacaaagtgacaaa 913
QY 781 agactgattgaaagaaagaaaggggtgaaagtggaaaaacagaccttctctcaaaaatc 840
Db 914 agactgattgaaagaaagaaaggggtgaaagtggaaaaacagaccttctctcaaaaatc 973
QY 841 atcttctcaatgtctctgaaacatgactatgggaactacactgctggtgctccaaacag 900
Db 974 atcttctcaatgtctctgaaacatgactatgggaactacactgctggtgctccaaacag 1033
QY 901 ctgagccacaaccaatgacagcatgctattggtccagggcgctcagcgaggtgagc 960
Db 1034 ctgagccacaaccaatgacagcatgctattggtccagggcgctcagcgaggtgagc 1093
QY 961 aacggacgctcgagagggcagggctgctgctgctgctctctctgcttctgacacgtg 1020
Db 1094 aacggacgctcgagagggcagggctgctgctgctgctctctctgcttctgacacgtg 1153
QY 1021 ctctcaaatctt 1032
Db 1154 ctctcaaatctt 1165

RESULT 6
AAZ47893

ID AAZ47893 standard; cDNA; 1693 BP.
XX
AC AAZ47893;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human protein encoding cDNA SEQ ID NO:3.
XX
KW Human; haematopoietic cell regulation; tissue generation; reparation;
KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmune; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..1164
FT /*tag= a
XX
PN WO9558668-A1.
XX
PD 18-NOV-1999.
XX
PE 13-MAY-1999; 99WO-JP02485.
XX
PR 14-MAY-1998; 98JP-0131815.
XX
PA (ONOR) ONO PHARM CO LTD.
XX
PI Fukushima D, Shibayama S, Tada H;
XX
DR WPI; 2000-062298/05.
DR P-PSDB; AAY57601.
XX
PT New polypeptides of human origin having cell regulatory, tissue
PT generation, coagulant and other activities -
XX
PS Claim 5; Page 42-45; 84pp; Japanese.
XX
CC The present sequence encodes a specifically claimed novel human protein.
CC The novel human protein can be used in therapeutic drugs for the
CC prevention and treatment of a broad range of disorders including
CC autoimmune and infection-related immunodeficiency, inflammatory
CC disorders, and neurological diseases. The novel protein is expected of
CC having haematopoietic cell regulatory activity, tissue generation/
CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC blood coagulation and thrombus activity, and receptor/ligand activity.
XX
SQ Sequence 1693 BP; 518 A; 432 C; 416 G; 327 T; 0 other;

Query Match 100.0%; Score 1032; DB 21; Length 1693;
Best Local Similarity 100.0%; Pred. No. 8e-310;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaaatgacaaattctatctcttgaggcaatcttcacgggctg 60
Db 130 atgaaaccatccagccaaaatgacaaattctatctcttgaggcaatcttcacgggctg 189
QY 61 gctgctctgtgtctcttccaaaggagtgcccgctgacgagcgagatgcaccttcccaaa 120
Db 190 gctgctctgtgtctcttccaaaggagtgcccgctgacgagcgagatgcaccttcccaaa 249
QY 121 gctatggacaacgtgacggtccggacgggggagagcgccacccctcaggtgcactattgac 180
Db 250 gctatggacaacgtgacggtccggacgggggagagcgccacccctcaggtgcactattgac 309
QY 181 aaccgggtacacccgggtgctgctgctaaacccgacacccatcctctatgctggaatgac 240
Db 310 aaccgggtacacccgggtgctgctgctaaacccgacacccatcctctatgctggaatgac 369
QY 241 aagtggtgctggtatccctcgctgctgctcttgagcaaccccaacgagtagacatc 300

Db 370 aagtggtccttgatcctcgcgtgtgtccttctgagcaacccaacagcagtaacgacatc 429
QY 301 gagatccagaacgtgagatgtatgacagagggccctaacacctgtcgtgtgcagacagac 360
Db 430 gagatccagaacgtgagatgtatgacagagggccctaacacctgtcgtgtgcagacagac 489
QY 361 aaccacccaagaacaccttaagggtccacacctattgtgcaagtatctcccaaatgtagag 420
Db 490 aaccacccaagaacaccttaagggtccacacctattgtgcaagtatctcccaaatgtagag 549
QY 421 attcttcagatatctccattaatgaagggaacaatatattagcctcaccctgcatacgaact 480
Db 550 attcttcagatatctccattaatgaagggaacaatatattagcctcaccctgcatacgaact 609
QY 481 gtagaccagagcctcagcttactctggagacacacatctctcccaagcgtgtgtgtgtg 540
Db 610 gtagaccagagcctcagcttactctggagacacacatctctcccaagcgtgtgtgtgtg 669
QY 541 agtgaagacgaatacttggaaattcagggcatcaccccgagagtcagggagactacagag 600
Db 670 agtgaagacgaatacttggaaattcagggcatcaccccgagagtcagggagactacagag 729
QY 601 tgcagtgccccaatgaacgtgtgcgcgcgcgcgtgtgtacgagagtaaggtcacccgtgac 660
Db 730 tgcagtgccccaatgaacgtgtgcgcgcgcgcgtgtgtacgagagtaaggtcacccgtgac 789
QY 661 tatccacatacatcttcagaagccaagggtacaggtgtcccgctgggacaaaaggggaca 720
Db 790 tatccacatacatcttcagaagccaagggtacaggtgtcccgctgggacaaaaggggaca 849
QY 721 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacaaggatgacaaa 780
Db 850 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacaaggatgacaaa 909
QY 781 agactgattgaaggaagaaaggggtgaaagtggaaaaaacagaccttctcctcaaaatc 840
Db 910 agactgattgaaggaagaaaggggtgaaagtggaaaaaacagaccttctcctcaaaatc 969
QY 841 atctcttcaatgtctctgaacatgaactatggaactacacttgctgtgcctccaacaag 900
Db 970 atctcttcaatgtctctgaacatgaactatggaactacacttgctgtgcctccaacaag 1029
QY 901 ctggggccaaccaatgccaagcatatgtattgtgccaggcgccgtcagcgaggtgagc 960
Db 1030 ctggggccaaccaatgccaagcatatgtattgtgccaggcgccgtcagcgaggtgagc 1089
QY 961 aacggcacgtcagagagggcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Db 1090 aacggcacgtcagagagggcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1149
QY 1021 ctctccaattt 1032
Db 1150 ctctccaattt 1161

RESULT 7

AAA88790
ID AAA88790 standard; cDNA; 1603 BP.
XX
AC AAA88790;

XX 19-FEB-2001 (first entry)

DE Human SECX cDNA Clone 11753149.0.6.

XX SECX; human; diagnosis; gene therapy; cell adhesion; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 92..1126
FT sig_peptide 92..190

FT mat_peptide /*tag= b
FT 191..1123
FT /*tag= c
PN WO200061754-A2.
XX
XX 19-OCT-2000.
PD
XX
XX 07-APR-2000; 2000WO-US09392.
PF
XX
XX 09-APR-1999; 99US-0128514.
PR 03-MAR-2000; 2000US-0128514.
XX
XX (CURA-) CURAGEN CORP.
PI Fernandez E, Vernet C, Shinkets R;
XX
XX WPI; 2000-679487/66.
DR P-PSDB; AAB19721.
XX

SECX polypeptides and the nucleic acids that encode them, useful for
diagnosing, preventing and treating e.g. cancers, inflammation,
arthritis and immunological disorders -

Claim 14; Fig 2; 143pp; English.

XX
CC The present sequence is that of SECX Clone 11753149.0.6, which
CC resembles rat neural cell adhesion molecule neurotrimin and human
CC oploid binding protein/cell adhesion molecule OBCAM. The clone
CC was initially identified in human foetal brain tissue. The
CC invention provides novel SECX polynucleotides (see AAA88789-804) and
CC the secreted or membrane-associated proteins encoded by them
CC (see AAB19720-34). SECX polynucleotides, polypeptides and antibodies
CC can be used in the detection, diagnosis and treatment (including
CC gene therapy) of a broad range of pathological states.
XX
SQ Sequence 1603 BP; 466 A; 422 C; 405 G; 310 T; 0 other;

Query Match 99.8%; Score 1030.4; DB 21; Length 1603;
Best Local Similarity 99.9%; Pred. No. 2.4e-309;
Matches 1031; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaaatgacaaattctatcttgggaactcttcaggcgctg 60
Db 92 atgaaaaccatccagccaaaatgacaaattctatcttgggaactcttcaggcgctg 151
QY 61 gctgctgtgtctcttccaagagagtgcccggtgcgcagcgagatgccacttcccaaa 120
Db 152 gctgctgtgtctcttccaagagagtgcccggtgcgcagcgagatgccacttcccaaa 211
QY 121 gctatgacaacgtgacggtccgcagggagagcgccaccctcaggtgacattgac 180
Db 212 gctatgacaacgtgacggtccgcagggagagcgccaccctcaggtgacattgac 271
QY 181 aaccgggtcaccgggtgtgctgtgctaaaccgcagcaaccatctctatgtgtggaatgac 240
Db 272 aaccgggtcaccgggtgtgctgtgctaaaccgcagcaaccatctctatgtgtggaatgac 331
QY 241 aagtggtcctgtgacccctcgcgtgtgtcttctgagcaacacccaacgcagtaacgacatc 300
Db 332 aagtggtcctgtgacccctcgcgtgtgtcttctgagcaacacccaacgcagtaacgacatc 391
QY 301 gagatccagaacgtgagatgtatgacagagggccctaacacctgtcgtgtgcagacagac 360
Db 392 gagatccagaacgtgagatgtatgacagagggccctaacacctgtcgtgtgcagacagac 451
QY 361 aaccacccaagaacaccttaagggtccacacctattgtgcaagtatctcccaaatgtagag 420
Db 452 aaccacccaagaacaccttaagggtccacacctattgtgcaagtatctcccaaatgtagag 511
QY 421 attcttcagatatctccattaatgaagggaacaatatattagcctcaccctgcatacgaact 480

Db 512 attctcagatatctccatlaatgaagggaacaatatatagcctcactgcatagaact 571
QY 481 ggtagaccagagcctaagcttacttgtagacacatctctcccaagcgttggcttgtg 540
Db 572 ggtagaccagagcctaagcttacttgtagacacatctctcccaagcgttggcttgtg 631
QY 541 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtaagggaactagag 600
Db 632 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtaagggaactagag 691
QY 601 tgcagtgctcccaatgaacgtggccgcccgtgtgtaagagagtaaaagtccaacgtgaac 660
Db 692 tgcagtgctcccaatgaacgtggccgcccgtgtgtaagagagtaaaagtccaacgtgaac 751
QY 661 tatccaccatacattcagaagccaagggtacaggtgtcccggtgggacaagaaggagaca 720
Db 752 tatccaccatacattcagaagccaagggtacaggtgtcccggtgggacaagaaggagaca 811
QY 721 ctgcagtgtagaagcctcagcagctccctcagcagaattccagtggtatcaagaagtacaaa 780
Db 812 ctgcagtgtagaagcctcagcagctccctcagcagaattccagtggtatcaagaagtacaaa 871
QY 781 agactgattgaaggaagaagggtgtgaaagtgtgaaacaagaccttctctcctcaaaactc 840
Db 872 agactgattgaaggaagaagggtgtgaaagtgtgaaacaagaccttctctcctcaaaactc 931
QY 841 atctcttcaatgtctctggaacatgactatgggaactacactgtgcgtggcctccacaag 900
Db 932 atctcttcaatgtctctggaacatgactatgggaactacactgtgcgtggcctccacaag 991
QY 901 ctggggccacacccaatggccagcatcatgtctattgttccagagcgccgtcagcgaggtgagc 960
Db 992 ctggggccacacccaatggccagcatcatgtctattgttccagagcgccgtcagcgaggtgagc 1051
QY 961 aacggcacgtcagaggaaggcagcgtctgtcgtctgtcctcttctgtcttgcacctg 1020
Db 1052 aacggcacgtcagaggaaggcagcgtctgtcgtctgtcctcttctgtcttgcacctg 1111
QY 1021 ctctcacaattt 1032
Db 1112 ctctcacaattt 1123

RESULT 8
ID AAA88791
AC AAA88791;
XX 19-FEB-2001 (first entry)
DT XX
DE Human SECX cDNA Clone 11753149.0.37.
XX
KW SECX; human; diagnosis; gene therapy; cell adhesion; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 501..1535
FT sig_peptide 501..599
FT mat_peptide 600..1532
FT /*tag= a
FT /*tag= b
FT /*tag= c
XX
PN WO200061754-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000MO-US09392.
XX
PR 09-APR-1999; 99US-0128514.
PR 03-MAR-2000; 2000US-0128514.

XX
PA (CURA-) CURAGEN CORP.
XX
PI Fernandez E, Vernet C, Shimkets R;
XX
DR WPI; 2000-679487/66.
DR P-PSDB; AAB19722.
XX
PS Claim 14; Fig 3; 143pp; English.
XX
CC The present sequence is that of SECX Clone 11753149.0.37, which
CC resembles rat neural cell adhesion molecule neurotrimin and human
CC oploid binding protein/cell adhesion molecule OBCAM. The clone
CC was initially identified in human foetal brain tissue. The
CC invention provides novel SECX polynucleotides (see AAB8789-804) and
CC the secreted or membrane-associated proteins encoded by them
CC (see AAB19720-34). SECX polynucleotides, polypeptides and antibodies
CC can be used in the detection, diagnosis and treatment (including
CC gene therapy) of a broad range of pathological states.
XX
SQ Sequence 2012 BP; 567 A; 503 C; 512 G; 430 T; 0 other;

Query Match 99.8%; Score 1030.4; DB 21; Length 2012;
Best Local Similarity 99.9%; Pred. No. 2.8e-309;
Matches 1031; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaaatgacaaattctatctcttggcgaattcttcagggtg 60
Db 501 atgaaaaccatccagccaaaatgacaaattctatctcttggcgaattcttcagggtg 560
QY 61 gctgctctgtgtctcttccaagaggtgccgtgcagcagcgagatgccacttcccaaa 120
Db 561 gctgctctgtgtctcttccaagaggtgccgtgcagcagcgagatgccacttcccaaa 620
QY 121 gctatggacaacgtgacggtcccgagaggggagagcgccaccctcagtgacatagac 180
Db 621 gctatggacaacgtgacggtcccgagaggggagagcgccaccctcagtgacatagac 680
QY 181 aaccgggtcacccgggtgtgacctgttaaaccggcagcaccatctctatgtcgggaatgac 240
Db 681 aaccgggtcacccgggtgtgacctgttaaaccggcagcaccatctctatgtcgggaatgac 740
QY 241 aagtgtgtccttgatctcctgcgtgtgtctcttctgagcaaccacaaagcagtaacgac 300
Db 741 aagtgtgtccttgatctcctgcgtgtgtctcttctgagcaaccacaaagcagtaacgac 800
QY 301 gagatccagaacgtgagatgttatgacgagggcccttacacctgtcgtgtgacagacagac 360
Db 801 gagatccagaacgtgagatgttatgacgagggcccttacacctgtcgtgtgacagacagac 860
QY 361 aaccacccaaaagacacctagaggtccacctcatgttgcagaatctcccaaatgtagag 420
Db 861 aaccacccaaaagacaccttagaggtccacctcatgttgcagaatctcccaaatgtagag 920
QY 421 attcttcagatatctccatlaatgaagggaacaatatattagcctcactgcatagcaact 480
Db 921 attcttcagatatctccatlaatgaagggaacaatatattagcctcactgcatagcaact 980
QY 481 ggtagaccagagcctaagcttacttgtagacacatctctcccaagcgttggcttgtg 540
Db 981 ggtagaccagagcctaagcttacttgtagacacatctctcccaagcgttggcttgtg 1040
QY 541 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtaagggaactagag 600
Db 1041 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtaagggaactagag 1100
QY 601 tgcagtgctcccaatgaacgtggccgcccgtgtgtaagagagtaaaagtccaacgtgaac 660

QY	659	actatccaccatacatcttcagaagccaagggtacagtggtccccgtgggacaanaaggga	718
Db	1134	actatccaccatacatcttcagaagccaagggtacagtggtccccgtgggacaanaaggga	1193
QY	719	cactgcagtggtgaagcctcacgagtcacctcacgagaattccagtgtacaagatgaca	778
Db	1194	cactgcagtggtgaagcctcacgagtcacctcacgagaattccagtgtacaagatgaca	1253
QY	779	aagagactgatgtgaagaaaggaagggtgtaaaagltgaaaaacagaccttccctccaaac	838
Db	1254	aagagactgat-t-aagaaagaaagggtgtaaaagltgaaaaacagaccttccctccaaac	1312
QY	839	tcaatctcttcaaatgtctcttgaacatgactatgygaactatacctltgctgtgccccaaca	898
Db	1313	tcaatctcttcaaatgtctcttgaacatgactatgygaactatacctltgctgtgccccaaca	1372
QY	899	agcttgggccacaaccaatgtcccagcatcatgtctaatttgtccaaggcgccgtacaagcgtga	958
Db	1373	agcttgggccacaaccaatgtcccagcatcatgtctaatttgtccaaggcgccgtacaagcgtga	1432
QY	959	gcaacgycacgctcgaggagggcaggctgcgtctgtgcgtccctctctgtlcttgacc	1018
Db	1433	gcaacgycacgctcgaggagggcaggctgcgtctgtgcgtccctctctgtlcttgacc	1492
QY	1019	tgcttctcaaattt 1032	
Db	1493	tgcttctcaaattt 1506	

RESULT	10
AAI57869	
ID	AAI57869 standard; cDNA; 1678 BP.
XX	
AC	AAI57869;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 72.
XX	
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW	leukemia; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US34263.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	
DR	WPI; 2001-442253/47.
DR	P-PSDB; AAM38713.
XX	

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 72; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

Sequence 1678 BP; 420 A; 468 C; 451 G; 339 T; 0 other;

Query Match	92.2%;	Score 952;	DB 22;	Length 1678;
Best Local Similarity	100.0%;	Pred. No. 5.7e-285;		
Matches 952;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	81	aggagtgcccgctgcgcagccgagatgtccaccttcgccaaagctatggaacgltgacggt	140
Db	222	aggagtgcccgctgcgcagccgagatgtccaccttcgccaaagctatggaacgltgacggt	281
QY	141	ccgcgcaggggagagcgcacccctcaggtgcaactattgacaaccggttcacccggtggc	200
Db	282	ccgcgcaggggagagcgcacccctcaggtgcaactattgacaaccggttcacccggtggc	341
QY	201	ctgcgtaaaccgcagcaccaactctctatgtctggagtgaacaagtgtgcctcgatcctcg	260
Db	342	ctgcgtaaaccgcagcaccaactctctatgtctggagtgaacaagtgtgcctcgatcctcg	401
QY	261	cgtgctcctctctgagcaacaccccaacgcagttacacgcatcgagatccagaacgttgatgt	320
Db	402	cgtgctcctctctgagcaacaccccaacgcagttacacgcatcgagatccagaacgttgatgt	461
QY	321	gtatgacgagggcccttacacctgtcgtgtgcagacagacacaccccaaaagacctctag	380
Db	462	gtatgacgagggcccttacacctgtcgtgtgcagacagacacaccccaaaagacctctag	521
QY	381	ggtccacctcaattgtgcgaagtatctcccaaatgtgagagattctctcagatatctccat	440
Db	522	ggtccacctcaattgtgcgaagtatctcccaaatgtgagagattctctcagatatctccat	581
QY	441	taatgaagggaacaatatattagcctcacctgcatagcaactgtgtagaccagagcctacggt	500
Db	582	taatgaagggaacaatatattagcctcacctgcatagcaactgtgtagaccagagcctacggt	641
QY	501	tacttgagagacaatctctcccaaaagcgtgttgctttgtgagtgaagacgaatacttga	560
Db	642	tacttgagagacaatctctcccaaaagcgtgttgctttgtgagtgaagacgaatacttga	701
QY	561	aattcagggcatcaccccgggagcagttcagggggactacgaagtgtcagttgcctccaatgacgt	620
Db	702	aattcagggcatcaccccgggagcagttcagggggactacgaagtgtcagttgcctccaatgacgt	761
QY	621	ggccgcgcgccggtgtgtacgcgagatgaaggtcacccgtgaactatccaccataatttcaga	680
Db	762	ggccgcgcgccggtgtgtacgcgagatgaaggtcacccgtgaactatccaccataatttcaga	821
QY	681	agccaagsgtacaaggtgtcccccgtgtggacaanaaggggacactgcaggtgtgaagcctcagc	740
Db	822	agccaagsgtacaaggtgtcccccgtgtggacaanaaggggacactgcaggtgtgaagcctcagc	881

QY 741 agtccctcagcagaattccagtgtgtacaaggatgacaaagacgtgattgaaggaaagaa 800
|||||
Db 882 agtccctcagcagaattccagtgtgtacaaggatgacaaagacgtgattgaaggaaagaa 941
QY 801 aggggtgaaagtggaaacagaccttctctctcaaaactcatctcttcaatgctctga 860
|||||
Db 942 aggggtgaaagtggaaacagaccttctctctcaaaactcatctcttcaatgctctga 1001
QY 861 acatgacctatgggaactacacttgcgtggcctccaacaagctgggccaaccaatgcca 920
|||||
Db 1002 acatgacctatgggaactacacttgcgtggcctccaacaagctgggccaaccaatgcca 1061
QY 921 catcatgtatttggccagggcgctcagcgaggtgagcaacggcagctcgaggaggc 980
|||||
Db 1062 catcatgtatttggccagggcgctcagcgaggtgagcaacggcagctcgaggaggc 1121
QY 981 aggcgtcgtctggcgtgctctctcttctgtcttgcacctgcttctcaaat 1032
|||||
Db 1122 aggcgtcgtctggcgtgctctctcttctgtcttgcacctgcttctcaaat 1173

RESULT 11

AAZ47894
ID AAZ47894 standard; cDNA; 939 BP.

AC AAZ47894;

DT 10-MAR-2000 (first entry)

DE Human protein encoding cDNA SEQ ID NO:5.

XX
KW Human; haematopoietic cell regulation; tissue generation; reparation;
KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmune; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..939
FT /*tag= a
FT /note= "no stop codon given"

PN WO958668-A1.

PD 18-NOV-1999.

PF 13-MAY-1999; 99WO-JP02485.

PR 14-MAY-1998; 98JP-0131815.

PA (ONOH) ONO PHARM CO LTD.

PI Fukushima D, Shibayama S, Tada H;

DR WPI; 2000-062298/05.

DR P-PSDB; AAY57602.

PT New polypeptides of human origin having cell regulatory, tissue
PT generation, coagulant and other activities
XX
PS Claim 4; Page 48; 84pp; Japanese.

CC The present sequence encodes a specifically claimed novel human protein.
CC The novel human protein can be used in therapeutic drugs for the
CC prevention and treatment of a broad range of disorders including
CC autoimmune and infection-related immunodeficiency, inflammatory
CC disorders, and neurological diseases. The novel protein is expected of
CC having haematopoietic cell regulatory activity, tissue generation/
CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC blood coagulation and thrombus activity, and receptor/ligand activity.

XX
SQ Sequence 939 BP; 245 A; 255 C; 249 G; 190 T; 0 other;

Query Match 91.0%; Score 939; DB 21; Length 939;
Best Local Similarity 100.0%; Pred. No. 4.5e-281;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 cgcagcgagatgccaccttccccaaagtatgacaacagtgacggtccgcgagggag 153
|||||
Db 1 cgcagcgagatgccaccttccccaaagtatgacaacagtgacggtccgcgagggag 60
QY 154 agcgccacctcaggtgacactattgacaacccgggtcacccgggtgacctgtaaccgc 213
|||||
Db 61 agcgccacctcaggtgacactattgacaacccgggtcacccgggtgacctgtaaccgc 120
QY 214 agcacatcctctatgctgggaatgacaagtgtgacctgatactcgcgtgctctctg 273
|||||
Db 121 agcacatcctctatgctgggaatgacaagtgtgacctgatactcgcgtgctctctg 180
QY 274 agcaaccccacaacgcagttacagatcgagatccagaacggtgattgtatgacgaggc 333
|||||
Db 181 agcaaccccacaacgcagttacagatcgagatccagaacggtgattgtatgacgaggc 240
QY 334 ccttacacctgtctggtgacagacacaccccaaaagacctctagggtccacctcatt 393
|||||
Db 241 ccttacacctgtctggtgacagacacaccccaaaagacctctagggtccacctcatt 300
QY 394 gtgcagtatctcccaaaattgtagagattcttcaagatatccattaatgaaggagac 453
|||||
Db 301 gtgcagtatctcccaaaattgtagagattcttcaagatatccattaatgaaggagac 360
QY 454 aatattagcctcacctgcatagcaactgtagaccagagcctaaggttacttggagacac 513
|||||
Db 361 aatattagcctcacctgcatagcaactgtagaccagagcctaaggttacttggagacac 420
QY 514 atctctccaaagcggtgtgcttgtgagtgaagacgaatacttggaaattcagggcacc 573
|||||
Db 421 atctctccaaagcggtgtgcttgtgagtgaagacgaatacttggaaattcagggcacc 480
QY 574 acccgggagcagtcaggggagctacgagtgctcctccaatgacgtggccgcgcctg 633
|||||
Db 481 acccgggagcagtcaggggagctacgagtgctcctccaatgacgtggccgcgcctg 540
QY 634 gtaaggagagtaaaaggtcacccgtgaactatccaccatacttccagaagccaagggtaca 693
|||||
Db 541 gtaaggagagtaaaaggtcacccgtgaactatccaccatacttccagaagccaagggtaca 600
QY 694 ggtgtcccccgtgggacaagaaggagacactgcaagtgtgaagcctcagcagctccctcagca 753
|||||
Db 601 ggtgtcccccgtgggacaagaaggagacactgcaagtgtgaagcctcagcagctccctcagca 660
QY 754 gaattccagtgtgtaacaagatgacaaagactgattgaaggaaagaagggtgaagt 813
|||||
Db 661 gaattccagtgtgtaacaagatgacaaagactgattgaaggaaagaagggtgaagt 720
QY 814 gaaaacagaccttctctctcaaaactcatcttcttcaatgtctctgaacatgactatgg 873
|||||
Db 721 gaaaacagaccttctctctcaaaactcatcttcttcaatgtctctgaacatgactatgg 780
QY 874 aactacacttggctggcctccaagaagctggggccaaccaatgccaagcatatgtatt 933
|||||
Db 781 aactacacttggctggcctccaagaagctggggccaaccaatgccaagcatatgtatt 840
QY 934 ggtccagggcgctcagcgaggtgagcaacggcagctcgaggagggcgctgctgg 993
|||||
Db 841 ggtccagggcgctcagcgaggtgagcaacggcagctcgaggagggcgctgctgctgg 900
QY 994 ctgctgcctctctctgtgtctgcaacctgcttctcaaat 1032
|||||
Db 901 ctgctgcctctctctgtgtctgcaacctgcttctcaaat 939

RESULT 12
AAA44536

ID AAA44536 standard; cDNA; 832 BP.
XX
AC AAA44536;
XX
DT 21-AUG-2000 (first entry)
DE Human secreted expressed sequence tag SEQ ID NO:1111.
XX
KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; antiparkinsonian;
KW antitumor; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200021991-A1.
XX
PD 20-APR-2000.
XX
PE 15-OCT-1999; 99WO-US24206.
XX
PR 15-OCT-1998; 98US-0104436.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-317938/27.
XX
PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (SESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
XX
PS Claim 1; Page 487-488; 803pp; English.
XX
CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 832 BP; 246 A; 217 C; 206 G; 163 T; 0 other;

Query Match 65.0%; Score 670.8; DB 21; Length 832;
Best Local Similarity 99.7%; Pred. No. 8.7e-198;
Matches 672; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 atgaaccatccagccaaaatgacacattctctcttcttggtcaatcttcaagggctg 60
Db 155 atgaaccatccagccaaaatgacacattctctcttcttggtcaatcttcaagggctg 214
QY 61 gctgtctgtgtctcttccaaagagtgccgtgcgacgagagatgccacttcccaaa 120
Db 215 gctgtctgtgtctcttccaaagagtgccgtgcgacgagagatgccacttcccaaa 274
QY 121 gctatggacaacgtgacggtccgacagggagagcgccacctcagtgactattgac 180
Db 275 gctatggacaacgtgacggtccgacagggagagcgccacctcagtgactattgac 334
QY 181 aaccggtcaccggtggtgcgtgctaaccgacgacacatctctatgctgggaatgac 240
Db 335 aaccggtcaccggtggtgcgtgctaaccgacgacacatctctatgctgggaatgac 394
QY 241 aagtgtgctgtgacgtcgtgctgctctctctctctctctctctctctctctctc 300
Db 395 aagtgtgctgtgacgtcgtgctgctctctctctctctctctctctctctctctc 454
QY 301 gagatccagaacgtggtgtgtatgacgagggcccttacacctgtcgtgtcagacagac 360
Db 455 gagatccagaacgtggtgtgtatgacgagggcccttacacctgtcgtgtcagacagac 514
QY 361 aaccacccaaagacctctaggtccacctcatgttgcaagtatctcccaaatgttagag 420
Db 515 aaccacccaaagacctctaggtccacctcatgttgcaagtatctcccaaatgttagag 574
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Db 635 ggtagaccagagcctacgttacttgtagacacatctctccaaagcgtgtgtgtg 694
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Db 695 agtgaagacgaactctggaattcagggcaccacccgagagcagtcagggactagag 754
QY 601 tgcagtgctcccaatgacgtggtgcggtgtgtgtagcagagtaaggtcaccgtgaac 660
Db 755 tgcagtgctcccaatgacgtggtgcggtgtgtgtagcagagtaaggtcaccgtgaac 814
QY 661 tatccaccatacat 674
Db 815 tatccaccatacat 828
RESULT 13
AA051015
ID AA051015 standard; cDNA; 3069 BP.
XX
AC AA051015;
XX
DT 17-MAY-1994 (first entry)
DE Rat opioid receptor gene.
XX
KW Transgenic; narcotics; analgesics; expression; antisense therapy;
KW analogue; derivative; degradation; chronic pain; cancer; morphine;
KW detection; diagnosis; addictions; ds.
XX
OS Rattus rattus.
XX
PN WO9321309-A.
XX
PD 28-OCT-1993.
XX

PF 29-MAR-1993; 93WO-US02913.
XX
PR 10-APR-1992; 92US-0866677.
XX
PA (LEEN/) LEE N M.
PA (LIPP/) LIPPMAN D.
PA (LOHH/) LOH H H.
XX
PI Lee NM, Lippman D, Loh HH;
XX
DR WPI; 1993-351719/44.

PT Transgenic animals and novel oligo-nucleotide constructs - useful
PT in diagnosis and treatment of addiction to narcotic analgesics
XX

PS Claim 5; Page 25-30; 49pp; English.

CC The sequence is that of the rat opioid receptor gene. The gene is
CC able to hybridise with endogenous mRNA for an opioid binding protein
CC to suppress expression of an opioid receptor gene. Transgenic
CC animals contg. the gene in reverse are useful in diagnosis and
CC treatment for addiction to narcotic analgesics. By admin. of
CC antisense fragments of the gene, chronic pain, such as in terminal
CC cancer patients can be treated without development of tolerance to
CC analgesics such as morphine. The gene may also be used
CC diagnostically to detect addicts.
CC See also AA051016-7.

XX
SQ Sequence 3069 BP; 803 A; 787 C; 661 G; 818 T; 0 other;

Query Match 51.9%; Score 536; DB 14; Length 3069;
Best Local Similarity 71.2%; Pred. No. 1.4e-155;
Matches 723; Conservative 0; Mismatches 290; Indels 3; Gaps 1;

QY 20 aaatgcacaattctatctcttggcaattctcaggggctgtgtctgtctctcc 79
DB 636 agatgtaccatcccgctactgtatcgtctctcgcgcaccactgacctgtcttcaccc 695
QY 80 aaggagtgcccgctgcagcagagatgcacccttcccaagctatggaacaagtgacgg 139
DB 696 caggagtgccggtgcgcagcagagatgcacccttcccaagctatggaacaagtgacgg 755
QY 140 tccgcaggggagagagcgccaccctcagtgacatttgacaacgggtcaccgggtgg 199
DB 756 tccgcaggggagagagcgccaccctcagtgacatttgacaacgggtcaccgggtgg 815
QY 200 cctggctaaccgcagcaccatctctatgtctgggaatgacaagtgtgcttgatctc 259
DB 816 cctggctaaccgcagcaccatctctatgtctgggaatgacaagtgtgcttgatctc 875
QY 260 gcgtgtctctctgagcaacaccccaacgagtaacgacatccagacgtgtgatg 319
DB 876 gagtgtatcatcttgttcaacaacgctaccagtaacgacatccagacgtgtgatg 935
QY 320 tgtatgacgagggcccttaacacctgtcgtgcagacaagacaacccaagaacctcta 379
DB 936 ttatgacgaggggtccgttacacctgtctgtgcagacaagacaacccaagaacctccc 995
QY 380 gggtccacctcattgtgcaagtatctcccaaatgtgagagattcttcagatatctcca 439
DB 996 gggtccacctcattgtgcaagtatctcccaaatgtgagagattcttcagatatctcca 1055
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DB 1116 tgacatggcgacacctgtcagtaacgaaggaagcggttgtgtgagtgagacgaataact 1175
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DB 1356 ctgctgtcccatgtgtgattccagtggttcaaggagataccaggttagccactggcc 1415
QY 797 agaaaggggtgaaagtgtgaaacacagacccttctcctcaaaactcattcttcaatgtct 856
DB 1416 tggatggcggtgagaattgagaacaaagccgcataatccacttgaatttctcaatgtct 1475
QY 857 ctgaacatgactatgggaactacacttcgtgtgacctccaacaagctggccaccacaatg 916
DB 1476 cagagaaggaattatgggaactataacctgtgtgcccacaacaagcttgggaaccacaatg 1535
QY 917 ccagcatcatgtctatttggtcagggccgctcagcgaagtgtgacaaagcagcagtcagga 976
DB 1536 ccagcatcaacctgtatgtggccttgagcagatcatgtatgtgttaactcggcctctagag 1595
QY 977 gggcaggtcgtctgt 1032
DB 1596 cactgt 1651

RESULT 14

AA051017
ID AA051017 standard; cDNA; 2179 BP.

XX
AC AA051017;

XX
DT 17-MAY-1994 (first entry)

XX
DE Rat opioid receptor gene.

KW Transgenic; narcotics; analgesics; expression; antisense therapy;
KW analogue; derivative; degradation; chronic pain; cancer; morphine;
KW detection; diagnosis; addictions; ds.

OS Rattus rattus.

XX
PN W09321309-A.

XX
PD 28-OCT-1993.

XX
PF 29-MAR-1993; 93WO-US02913.

XX
PR 10-APR-1992; 92US-0866677.

XX
PA (LEEN/) LEE N M.

XX
PA (LIPP/) LIPPMAN D.

XX
PA (LOHH/) LOH H H.

XX
PI Lee NM, Lippman D, Loh HH;

XX
DR WPI; 1993-351719/44.

XX
PT Transgenic animals and novel oligo-nucleotide constructs - useful
PT in diagnosis and treatment of addiction to narcotic analgesics
XX

PS Claim 5; Page 34-7; 49pp; English.

CC The sequence is that of the rat opioid receptor gene. The gene is
CC able to hybridise with endogenous mRNA for an opioid binding protein
CC to suppress expression of an opioid receptor gene. Transgenic
CC animals contg. the gene in reverse are useful in diagnosis and
CC treatment for addiction to narcotic analgesics. By admin. of

CC antisense fragments of the gene, chronic pain, such as in terminal
CC cancer patients can be treated without development of tolerance to
CC analgesics such as morphine. The gene may also be used
CC diagnostically to detect addicts.
CC See also AA051015-6.

Sequence 2179 BP; 548 A; 533 C; 494 G; 604 T; 0 other;

Query Match	50.28;	Score 518.2;	DB 14;	Length 2179;
Best Local Similarity	72.18;	Pred. No. 3.8e-150;		
Matches 689; Conservative	0;	Mismatches 263;	Indels 3;	Gaps 1;

QY	81	aggagtgcccgctgcgcagcgagatgccaacttccccaaaagtatggaacaagtgcaggt	140
Db	378	aggagtgcccggtgcgcagcgagatgccaacttccccaaaagtatggaacaagtgcaggt	437
QY	141	ccgcgcagggggagagcgccaccctcaggtgcacatatgacaacccggtgcacccggtg	200
Db	438	ccgcgcagggggagagcgccaccctcaggtgcacatatgacaacccggtgcacccggtg	497
QY	201	ctggtcaaaacccgcagcaccatcctctatgctggtgaatggaacaagtgtgctgctcg	260
Db	498	ctggtcaaaacccgcagcaccatcctctatgctggtgaatggaacaagtgtgctgctcg	557
QY	261	cgtgtctcctctgtgagcaacaccccaacgcaggtacagcatcgagatccgaacgtgtgt	320
Db	558	agtgtatcatctgtgtcaacacgcctacccagtagcatgatacatgataccagaatgtgtgt	617
QY	321	gtatgacgagggcccttacacctctcgtgtgcagacagacaaccccaaaagcctctag	380
Db	618	ttatgacgagaggtcccgtaacacctgctctgtgcagacagacaatacaccccaacccctccg	677
QY	381	gtgccaccctcatgtgtgcaagtatctcccaaaattgtagagattcttcagatatctcat	440
Db	678	gtgccaccctcatgtgtgcaagtatctcccaaaattgtagagattcttcagatatctcat	737
QY	441	taatgaaagggaacataattagccttcacctgcatagcaactggtagaccagagcctaaggt	500
Db	738	gaatgagataagcaggtgtgacctgtgtatctcgaactgtgcagaccagacaacaacag	797
QY	501	tacttggagacacatactctccca--aagcgglttgcttgtgtgagtgaagcaataact	557
Db	798	gacatggtgcacacactgtgcagtcaagaaagcgcaaggcttctgtgtgaagtgaataact	857
QY	558	ggaaatlcagggcatcaccccggtgagcaggtcagggacatcaggtgcagctcccaatga	617
Db	858	ggaaatctcagacatacaacgcgagccaactctgagagatgagtgcagcgcccttgaatga	917
QY	618	cgtggtccgcgcgcgtgtgtacggagagttaaaggtcacccgtgaactatccacataacttc	677
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Db	978	aaaagcgaaagaacaactggtgttcttcagtaggcagaagggcatcctgtagctgtgaagcctc	1037
QY	738	agcagtcctccctcaagcagaatctccagttgtgtacaagagatgacaaagactgattgaagaaa	797
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QY	858	tgaacatgactatgggaacttacaacttgcgtgtgacctccaacaaagcttgggccaacgaatgc	917
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QY	918	cagcatcatgtctatttgtgtccaggcgccggtcagcgaggtgtgagcaacgcgcaagctcagagag	977
Db	1218	cagcatcatccctgtatgtggtccttgagcaggtcatgtgagtgtgtaaactcggtcctlaagac	1277

QY	978	gcaagsgctgcgcgtctygtcgtgcctcttccttgcttgcacctgctctccaattt	1032
Db	1278	actygcttgtctctcgctctccaggacatctctttgcccaactctctcatcaagt	1332

RESULT	15
AAQ51016	
ID	AAQ51016 standard; cDNA; 2337 BP.

AC AAQ51016;

DT 17-MAY-1994 (first entry)

Rat opioid receptor gene.

KW Transgenic; narcotics; analgesics; expression; antisense therapy;
KW analgesic administration; transgene expression

KW detection; diagnosis; addicts; ds.
XY

05 Rattus rattus.
yy

PN W09321309-A.
XY

PD 28-OCT-1993.
XX

PF 29-MAR-1993; 93WO-US02913.
XX

PR 10-APR-1992; 92US-0866677.
XX

PA (LEEN/) LEE N M.
PA (LIPP/) LIPPMAN D.
PA (LOHH/) LOH H H.

PI Lee NM, Lippman D, Loh HH;
PI

DR WPI; 1993-351719/44.

Transgenic animals and novel oligo-nucleotide constructs - useful in diagnosis and treatment of addiction to narcotic analgesics

PS Claim 5; Page 30-3; 49pp; English.

CC The sequence is that of the rat opioid receptor gene. The gene is
CC able to hybridise with endogenous mRNA for an opioid binding protein
CC to suppress expression of an opioid receptor gene. Transgenic
CC animals contg. the gene in reverse are useful in diagnosis and
CC treatment for addiction to narcotic analgesics. By admin. of
CC antisense fragments of the gene, chronic pain, such as in terminal
CC cancer patients can be treated without development of tolerance to
CC analgesics such as morphine. The gene may also be used
CC diagnostically to detect addicts. See also AA051015-7.

SD Sequence 2337 BP; 581 A; 578 C; 520 G; 658 T; 0 other;

Query Match	50.2%;	Score 518.2;	DB 14;	Length 2337;
Best Local Similarity	72.1%;	Pred. No. 3.9e-150;		
Matches 689;	Conservative 0;	Mismatches 263;	Indels 3;	Gaps 1;

[illegible]

```

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QY 321 gtatgacgaagggcccttacacctgtcgtgacagacagacacacccaaagacctag 380
Db 787 ttaigacgaaggtccgtacacctgtctgtgacagacagacacacccaaagacctccg 846
QY 381 ggtccacctcatgtgcaagtaatcccaaatgttagagattcttcagatatctccat 440
Db 847 ggtccacctcatgtgcaagtaatcccaaatgttagagattcttcagatatctccat 906
QY 441 taatgaagggaacaatatattagccttcacactgcatagcaactgttagaccagagcctacgt 500
Db 907 gaatgagataaagcagtgtagacctgttagatgtctgcaattggcagaccagaaacacag 966
QY 501 tacttgagaacacatctctccca--aagcggttggtcttgtgagtgaagacgaatctt 557
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Db 1327 agaagaagattatgggaactataacctgtgtggccacaacaagcttgggaaccaatgc 1386
QY 918 cagcatcatgctatttggtcacagggcgctcagcgaggtgagcaagcgacgctcgagagag 977
Db 1387 cagcatcacacctgtatggcctggagcagtcattgtatgtgttaactcgcccttagagc 1446
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Search completed: July 11, 2002, 23:01:01
 Job time: 8929 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 19:07:41 ; Search time 4995.85 Seconds

(without alignments)
4322.825 Million cell updates/sec

Title: US-09-700-397-1

Perfect score: 1032

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

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2	804.8	78.0	2040	10	RNU16845	U16845 Rattus norv
3	787.2	76.3	1410	10	AF282980	AF282980 Mus muscu
4	642.8	62.3	1058	5	AF292935	AF292935 Gallus ga
5	640.8	62.1	1257	5	GGCEPUI	Z72497 G.gallus mr
6	635.8	61.6	1035	5	AB011810	AB011810 Gallus ga
7	623.6	60.4	1638	12	AF271233	AF271233 Synthetic
8	604.8	58.6	1013	5	AF292936	AF292936 Gallus ga
9	566.6	54.9	1533	5	FFNINHS5A	Y08170 Gallus gall
10	547.2	53.0	1556	5	AF292934	AF292934 Gallus ga
11	540.6	52.4	2593	4	BTOBCAM	X12672 Bovine mRNA
12	536	51.9	3069	10	RATCALMA	M88709 Rattus norv
13	534.2	51.8	1478	9	HUMOBAM	L34774 Human (clon
14	518.2	50.2	2179	10	RATCALMB	M88710 Rattus norv
15	518.2	50.2	2337	10	RATCALMC	M88711 Rattus norv
16	464.2	45.0	2935	12	AF271618	AF271618 Synthetic
17	464.2	45.0	3216	5	GGCEPUS	AJ225897 Gallus ga
18	434.4	42.1	756	12	AF271232	AF271232 Synthetic
19	357.8	34.7	1107	5	GGLAMP9	Z94718 G.gallus mr
20	355	34.4	1158	5	GGLAMP19	Z94720 G.gallus mr
21	353.4	34.2	2050	5	GGEI9SPRO	Y08171 Gallus gall
22	348.4	33.8	1194	5	GGLAMP11	Z94719 G.gallus mr
23	340.6	33.0	924	6	AR030579	AR030579 Sequence
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28	340.6	33.0	1238	10	RNU31554	U31554 Rattus norv
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31	337.4	32.7	945	6	AR030580	AR030580 Sequence
32	333.8	32.3	861	6	AR030582	AR030582 Sequence
33	330	32.0	452	6	AX079423	AX079423 Sequence
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39	235.6	22.8	203572	9	AC016769	AC016769 Homo sapi
40	207.6	20.1	786	5	GGA132998	AJ132998 Gallus Ga
41	205.6	19.9	71276	2	AC102028	AC102028 Mus muscu
42	176.6	17.1	116069	2	AP000784	AP000784 Homo sapi
43	176.6	17.1	123320	9	AP000863	AP000863 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AF126426
DEFINITION Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION AF126426
VERSION AF126426.1 GI:7158997
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1839)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.

TITLE Cloning and identification of human neurotrimin full length cDNA

REFERENCE 2 (bases 1 to 1839)

Unpublished

AUTHORS Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.

TITLE Direct Submission

JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical

Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China

FEATURES
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1.1839
/gene="HNT"
265.1299
CDS /gene="HNT"
/note="similar to Rattus norvegicus neurotrimin"
/codon_start=1
/product="neurotrimin"
/protein_id="AAF37591.1"
/db_xref="GI:7158998"

BASE COUNT 464 a 506 c 503 g 366 t
ORIGIN

Query Match 92.1%; Score 950.4; DB 9; Length 1839;
Best Local Similarity 99.9%; Pred. No. 4.2e-253;
Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LVVHLHLKF"
LSKLIFNVSEHDYGNVTCVANSNKLGHNTASIMLFGPAVSEVNSGTSRRAGCIVMLLP
VNYPEYISEAKGTGVPVGOKGLQCEASAVPSAEFQWFKDKRLVEGKGVKVENRPF
GREPEVTWRHISPKAVGFVSEDEYLEIQITREOSGECSANDVAPVRRVKT
ONVDVYDEGPTQSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICIAI
VTVROGESATLRCTIDNRVTRVAMLNRSITLYAGNDKWCIDPRVILSNTOYSIEI
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VTVROGESATLRCTIDNRVTRVAMLNRSITLYAGNDKWCIDPRVILSNTOYSIEI
/db_xref="GI:7158998"

QY 81 agaggtgcccgtgagcagcgagatgcccaccttcccaaaagtctatgaaacgtgacgt 140
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QY 141 ccgagcagggagagcgccacctcaggtgcactattgacaaccgggtgacccgggtggc 200
DB 405 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 464
QY 201 ctggctaaaccgagcaccatctctatctggaatgacaagtgtgctgacccctg 260
DB 465 CTGGCTAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524
QY 261 cgtggtccttctgagcaacacccaaacgagctacagcagatgacgaacgtgacgt 320
DB 525 CGTGGTCTTCTGAGCAACACCAAGCAGTACAGATCGAGATCGAAGACGTGATGT 584
QY 321 gtagcagagggcccttaccactgctcgtgagcagacagacaaccacaaagacccctag 380
DB 585 GTATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 644
QY 381 ggtccacctcattgtgcaagtattcccaaaattgtgagatttcttcagatatctccat 440
DB 645 GGTCCACCTCATTTGTGAGATATCTCCCAAAATTGTGAGATTTCTTCAGATATCTCCAT 704
QY 441 taatgaaggaacatatattagcctcactgcatagcactgtagacagagacccctacgt 500
DB 705 TAATGAAGGAGACATATATAGCCTCAGCTGACCACTGTTAGACCAAGACCTTACGGT 764
QY 501 tacttgagagacacatctctcccaaaagcgttggcttgtgagtgaaagacgaattctga 560
DB 765 TACTTGAGAGACATCTCTCCCAAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGA 824
QY 561 aattcagagcatcaaccgggagcagtgagggagtgacagtgacgtgacctccaatgacgt 620
DB 825 AATTCAAGGAGCATCACCCGGGAACAGTCAAGGAGTACAGTACAGTACAGTACAGTACAG 884
QY 621 ggcgcgcgcgcgtgtgtagagagagtaaggtcacctgtaactatccacatattctaga 680
DB 885 GGCCGCGCCCGTGTGAGAGAGAGTAAAGGTACACCGTGAACATACCATATTTCAGA 944
QY 681 agccaaggttacaggtgtcccggtgacaaaagggagacactgagtgatgaagcctcagc 740
DB 945 AGCCAAGGTTACAGGTGTCCCGGTGAGCAAAAAGGGGACACTGCACTGTGAGACCTTCAGC 1004
QY 741 agtccctcagcagaattccagtgtgtaacaagatgacaaaagactgattgaaggaagaa 800
DB 1005 AGTCCCTCAGCAGAAATTCAGTGTGTAACAAGATGACAAAAGACTGATTGAAGGAAAGAA 1064

QY 801 aggggtgaaagtgaacagacaccccttccctcctcaaaactatcttctaatgtctcga 860
DB 1065 AGGGGTGAAAGTGAAGAAACAGACCTTTCTCTCAAAACTCATCTTCTCAATGTCTGA 1124
QY 861 acatgaactatgggaactacacttgcgtgctcccaacagctgggccaaccaatgccaag 920
DB 1125 ACATGACTATGGGAACCTACACTTGCCTGCTCCACACAGCTGGGCCACCAATGCCAG 1184
QY 921 catcatgctattgtgtccaggcgccgtcagcgaggtgagcaacgagcagctcgagagggc 980
DB 1185 CATCATGCTATTGTGTCAGGCGCCGTCAGGAGGTGAGCAACGGCAGTGCAGAGGCGC 1244
QY 981 aggtcgtctgctgctgctcctctctggtcttgacactgctctcctcaattt 1032
DB 1245 AGGCTCGCTGTGCTGCTGCTCTCTCTGCTGTGACACCTGCTTCTCAATTT 1296

RESULT 2

RNU16845 2040 bp mRNA linear ROD 26-MAY-1995
LOCUS Rattus norvegicus neurotrimin mRNA, complete cds.
DEFINITION U16845
ACCESSION U16845.1 GI:755184
VERSION U16845.1
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 2040)
AUTHORS Struyk, A.F., Canoll, P.D., Wolfgang, M.J., Rosen, C.L., D'Eustachio, P. and Salzer, J.L.
TITLE Cloning of neurotrimin defines a new subfamily of differentially expressed neural cell adhesion molecules

JOURNAL J. Neurosci. 15 (3), 2141-2156 (1995)
MEDLINE 95198094
REFERENCE 2 (bases 1 to 2040)
AUTHORS Salzer, J.L.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical Center, 550 First Avenue, New York, NY 10016, USA

FEATURES location/Qualifiers
1..2040
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
484..1518
/note="neural cell adhesion molecule"

CDS
/codon_start=1
/product="neurotrimin"
/protein_id="AA67445.1"
/db_xref="GI:755185"

/translation="MGVCGYLFPLPKCLVNVSLRLLFLVPTGVPVRSQDATFPKAMDN
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ONVDVYDEGPTQSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICIAI
GREPEVTWRHISPKAVGFVSEDEYLEIQITREOSGEYECASNDVAPVRRVKT
VNYPEYISEAKGTGVPVGOKGLQCEASAVPSAEFQWFKDKRLVEGKGVKVENRPF
LSRLTFNVSEHDYGNVTCVANSNKLGHNTASIMLFGPAVSEVNSGTSRRAGCIVMLLP
LVVHLHLKF"

BASE COUNT 504 a 544 c 551 g 441 t
ORIGIN

Query Match 78.0%; Score 804.8; DB 10; Length 2040;
Best Local Similarity 90.3%; Pred. No. 1.3e-212;
Matches 860; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 81 agaggtgcccgtgagcagcgagatgcccaccttcccaaaagtctatgaaacgtgacgt 140
DB 564 AGGAGTGCCTGCGGAGAGGAGATGCCACTTTCACAAAGCTATGAGACAGTGACGGT 623
QY 141 ccgagcagggagagcgccacctcaggtgacactattgacaaccgggtgacccgggtggc 200

Db 624 CAGGCAAGGGGAGAGGCCACCCTCAGGTGCACAATGACACCGAGTCAACCCGGGTGCC 683

QY 201 ctggctaaaccgcagcaaccatctctatgtcgtgaatgacaagtgtgcctgtatcctcg 260

Db 684 CTGGCTAAACCGCAGTACCATCTCTATGCTGGAATGACAGTGTGCTAGATCCTCG 743

QY 261 cgtgtcctctctgagcaaccaccaagcagctacagatcgagatccagaacgtgtatgt 320

Db 744 TGTGTTCTCTCTGAGTAACACCCAGACCCAGTACAGCATGTAGATCCAGATGTGATGT 803

QY 321 gtaagcagagggcccttacacctgtcgtgacagacacaccccaaacacctctag 380

Db 804 GTATGATGAGGGCCCTTATACCTGCTCGGTGCAGACAGACACACCCCTAGACCTCCAG 863

QY 381 ggtccacctcattgtgcaagtatctcccaaatgttagagattcttcagatatctccat 440

Db 864 GGTCCACCTCATTTGTACAGATATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCAT 923

QY 441 taatgaagggaacaataattagcctcacctgcatagcaactgtagaaccagacctaggt 500

Db 924 TAATGAAGGGGAACAACATCAGCCTCATTGCAATAGCCACAGTAGACCCGGAGCCTACAGT 983

QY 501 taattgagagacacatctctcccaaacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 560

Db 984 AACCTGGAGACATATTTCTCCCAAGCTGTGCTTTGTGAGTAGAGATGATACCTGGA 1043

QY 561 aattcagggcatcaccggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 620

Db 1044 GATCCAGGGCATCACTCGGAGAGAGTCAAGCGCATGTAGTGCACGCGCCCAACGACGT 1103

QY 621 ggcgcgccccgtgtgtaagagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaag 680

Db 1104 GGCAGACACAGTCTGTACGAGAGTGAACGTACCCGTGACATATCCACCATACATCTCAGA 1163

QY 681 agccaaggtacagagtggtcccgctgggacaaagggagacactgcatgtgtgaagcctcagc 740

Db 1164 AGCTAAGGGTACAGGTGTCCCGCTGGGAGAGGGGACTGTCTGAGTGAAGCCTCGGC 1223

QY 741 agtccctcagcagaattccagtggtacagagatgacaaagactgtatgaagaaagaa 800

Db 1224 AGTCCCTCAGCAGAAATTTCACTGTTCAAGGATGACAAAGACTGTGTGAAGGGAAGAA 1283

QY 801 aggggtgaagtaaaacagacacttccctcacaactcattcttcaatgtctctga 860

Db 1284 GGGAGTCAAGTGAAGAAACAGACCTTCTTCAAGACTCCTTTTCAACGTCTCTGA 1343

QY 861 acatgactatgggaactacactgtcgtggtcccaacagctggccacccaatgtccag 920

Db 1344 ACACGACTATGGGACTACACATGTGTGCAACCAAGTTGGCCACACCAATGCCAG 1403

QY 921 catcatgctattgtgtccagggccgtcagcagagtgtagcaacggcagctcagagagc 980

Db 1404 CATCATGTCTATTGGCCAGAGTGTGTGTCAGCGAGGTCAACATGGGACGTCAAGAGGCG 1463

QY 981 aggtcgtctgt 1032

Db 1464 AGGCTGCATTTGGCTCTCCCTCTTCTGTTTACACCTGCTCTCAAAATTT 1515

RESULT 3

AF282980 1410 bp mRNA linear ROD 01-FEB-2001

LOCUS AF282980

DEFINITION Mus musculus neurotlimin mRNA, complete cds.

ACCESSION AF282980

VERSION AF282980.1 GI:12642539

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1410)

AUTHORS Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.

TITLE Cloning and expression of mouse neurotlimin gene in the developing

JOURNAL nervous system

REFERENCE 2 (bases 1 to 1410)

AUTHORS Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea

FEATURES

source location/Qualifiers

1. 1410

/organism="Mus musculus"

/strain="ICR"

/db_xref="taxon:10090"

/tissue_type="brain"

/dev_stage="adult"

1. 1035

/note="Similar to Rattus norvegicus neurotlimin"

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/product="neurotlimin"

/protein_id="AAK00276.1"

/db_xref="GI:12642540"

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BASE COUNT 369 a 365 c 368 g 308 t

ORIGIN

Query Match 76.3%; Score 787.2; DB 10; Length 1410;

Best local Similarity 89.2%; Pred. No. 9.5e-208;

Matches 849; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 81 aggaagtccccgcygcagcagagatgcccacttccccaaagctatgagacaagtgagagt 140

Db 81 AGGAGTGCCTGGTGGTAGCGGAGATGCTTACCTTTCCCAAGCTATGACAAACGTGACGGT 140

QY 141 ccgagaggggagagcgccaccctcagtgacatattgacaacccgggtcaccgggtgac 200

Db 141 CAGGCAGGGGGAGCGCCACCTCAGGTGACCAATTGACAAACCGAGTACCCGGGTGCG 200

QY 201 ctggtctaaaccgcagcaccatctctatgtcgtgaatgacaagtgtgtgctgtatcctcg 260

Db 201 CTGGCTAAACCGCAGTACCATCTCTATGCTGGAATGACAAAGTGTGCTAGATCCTCG 260

QY 261 cgtgtcctctctgagcaaccaccaagcagctacagatcgatccagaacgtgtatgt 320

Db 261 TGTGCTCTCTCTGAGTAACACCCAGACCCAGTACAGCATGTAGATCCAGATGTGATGT 320

QY 321 gtaagcagagggcccttacacctgtcgtgacagacacaccccaaacacctctag 380

Db 321 GTACGATGAGGGCCCTTATACCTGCTCGGTACAGATGACAAATCACCCTAAGACCTCCAG 380

QY 381 gttccacctcattgtgcaagtatctcccaaatgttagagattcttcagatatctccat 440

Db 381 GGTCCACCTCATTTGTACAGATATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCAT 440

QY 441 taatgaagggaacaataattagcctcacctgcatagcaactgtagaaccagacctaggt 500

Db 441 TAATGAAGGGGAACAACATCAGCCTCATTGCAATAGCCACAGTAGAGCGGAGCCTACAGT 500

QY 501 taattgagagacacatctctcccaaacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 560

Db 501 AACCTGGAGACATATTTCTCCCAAGGCTGTGCTTTGTGAGTAGAGATGATACCTGGA 560

QY 561 aattcagggcatcaccggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 620

Db 561 GATCCAGGGCATCACTCGGAGAGAGTCAAGCGCATGTAGTGCACGCGCCCAACGACGT 620

QY 621 ggcgcgccccgtgtgtaagagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaag 680

Db 621 GGCGGCACCAAGTGGTACCAAGAGTGAAGGTACCGTGAACCTATCCACCACTTCTCAGA 680
QY 681 agccaagggtaccggtgtcccccgtgggacaaaaggagacactgagtgtaagcctcagc 740
Db 681 AGCTTAAGGGCAGAGGTGTCCCGTGGGGCAGAAAGGGAGCTCTGAGTGAAGCTCCGC 740
QY 741 agtccctcagcagaaltccagtggtacaaagatgacaaaagactgatgaaagaa 800
Db 741 AGTCCCTTACAGCAAGATTTCATAGTGTCAAGGATGACAAAGACTGTGCAAGGAAGAA 800
QY 801 aggggtgaaagtggaacacagaccccttcctcaaatcatcttctcaatgtctctga 860
Db 801 GGGAGTCAAAAGTGGAAAAACAGACCTTCTCTTCAAACTCACTTTTCAACGCTCTGCA 860
QY 861 acatgactatgggaactacactgtgctgctcccaacaaagtgggacacccaatggcag 920
Db 861 ACATGACTATGGGAACACTACACATGTGTGGCTCCACACAGCTGGGTGACACCAACGCCAG 920
QY 921 calcatgtattgtgtccagcgcgctcagcagagtgtgagcaacgcagctcgaagagggc 980
Db 921 CATCATGTATTGTGTCCCGGTGCTGTGAGTGAAGGTCAACAATGGGACATCAACAGGGC 980
QY 981 aggtgtgctgt 1032
Db 981 AGGCTGCAATTGGCTCTCCCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1032

RESULT 4
AF292935 1058 bp mRNA linear VRT 24-AUG-2000
LOCUS AF292935
DEFINITION Gallus gallus CEPU-Se alpha 2 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292935
VERSION AF292935.1 GI:9887384
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1058)
AUTHORS Lodge, A.P., McNamee, C.J., Howard, M.R., Reed, J.E. and Moss, D.J.
TITLE Characterisation of CEPU-Se, a secreted isoform of the IgLON family protein CEPU-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1058)
AUTHORS Lodge, A.P. and Moss, D.J.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The University of Liverpool, Ashton Street, Liverpool, Merseyside L69 3GE, UK

FEATURES
source Location/Qualifiers
1..1058
/organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="brain"
/dev_stage="E18"
1..1058
/gene="CEPU-Se"
52..993
/gene="CEPU-Se"
/note="IgLON family protein; secreted form of CEPU-1"
/codon_start=1
/product="CEPU-Se alpha 2 isoform"
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VRQESATLRCSVDNRVTRVAMLRSSILYAGNDKWLDPVVLANIKTQYSIQIH
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PDPTTWKRHISPKAVGFISEDEYLETITREQSGEYECASNDVAAPVQRVKTVN
YPPYISDAKSTGVGOKGILMCEASAVPSADFQWYKDKRLAEGQKGLVENKAFPS
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BASE COUNT 250 a 320 c 310 g 178 t
ORIGIN

Query Match 62.3%; Score 642.8; DB 5; Length 1058;
Best Local Similarity 80.5%; Pred. No. 1.3e-167;
Matches 752; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 3 gaaaccatcagccaaaatgacaaattctctctgtggcaatcttcaggggtgtgc 62
Db 48 GAAATAGGCCAGGGGAAATGACGACACCCCTCTCATGGGTGATCTTCGCCGGATGCC 107
QY 63 tgcctgtgtctctccaaagagtgccggtgagcagcagcagcagcagcagcagcagc 122
Db 108 CGCACTCTCTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAGC 167
QY 123 tatgacacagtgacggtccggcaggggagagcgcacccctcagtgactatgacaa 182
Db 168 TATGACACAGTGACTGTGCGGCAAGGGGAGAGTGCCACGCTCAGGTGCTCCGTGACAA 227
QY 183 ccggttcaaccggtgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 242
Db 228 CCGGCTCACCCCGGTGCGCTGCTGGAACCCGACGACGATCTCTATGCGGCAATGACAA 287
QY 243 gtgtgtcctgtgtatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 302
Db 288 GTGTGTCTTGACCCCGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 347
QY 303 gatccagaacgt 362
Db 348 GATCCACGACGTGACGCTGTACGATGAGAGGGCCCTACACCTGCTCCGTGACAGACAA 407
QY 363 ccacccaagaacctcagtggtccacctcatgtgtgaagtatctccaaatgtgaagt 422
Db 408 TCACCCCAAGACATCTGCGCTGACCTCATTTGTGAAGTGTGCGGAAATTTACCGAGAT 467
QY 423 ttctcagatatctccaatatgaaggaacaaatatagcctcactgtcatagcaactgtg 482
Db 468 CTCTTCTGACATCTCCATCATGAGGTGGCAACGTCAAGCTTCACTGATAGCCACGGG 527
QY 483 tagaccagaagcctcagtggtccacctcatgtgtgaagtatctccaaatgtgaagt 542
Db 528 CAGGCCAAGCCCAACATCACTGAGACACATCTGCCCCAAGCTGTGGGCTTTCATCAG 587
QY 543 tgaagcagaatcacttgaagaattcagggcatcaccgggagcagtgagtgactacgagt 602
Db 588 CGAGGACGAGTACCTGGAGATCACAGGCATCACAGAGGAGCAGTGGGGCAGTACGAGTG 647
QY 603 cagtgctccaatgaagtgccgcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 662
Db 648 CAGTGCCTCCAACGAGCTGGCCGCTGTGCTGACGAGGAGTCAAAAGTCAACCTCAACTA 707
QY 663 tccaccatacattgaagaagcagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 722
Db 708 CCCACCGTACATCTGGATGCGAAGACACCCGCTGTGCGGCGGAGAGGGCATCTCT 767
QY 723 gcaagtgtgaagcctcagcagtgccctcagcagaattccagtggtgtacaaagatgacaa 782
Db 768 GATGTGTGAAGCCTCCGCTGTGCTCTGTGACTTCCAGTGTGACAAAGAGCACAAGCG 827
QY 783 actgattgaaggaagaaggggtgaagtgtgaagaacagacatttctctcaaaactcat 842
Db 828 GCTGCTGAAGGACAGAAAGGGCTGAAGGTGGAATAACAAAGCCCTTCTTCCCGACTGAC 887
QY 843 ctcttcaatgtctctgaacatcatatgtggaactacactgtgctgtgtgtgtgtgtgtgt 902
Db 888 TTCTTCAACAGTCTCCGAGCAGGACTACGCACTACACCTGCGTGGCTTCAACACGAGCT 947
QY 903 gggcacaaccaatgtccagcatatgtctatttgt 936
Db 948 AGGAACAACCAACGCCAGCATGATCTTATGTT 981

RESULT 5
GGCEPUI

LOCUS	GGCEPU1	1257 bp	mRNA	linear	VRT 29-APR-1998
DEFINITION	G.gallus mRNA for CEPU-1.				
ACCESSION	Z72497				
VERSION	Z72497.1 GI:1325950				
KEYWORDS	Brain; CEPU-1; glycoprotein; GPI-anchor protein.				
SOURCE	chicken.				
ORGANISM	Gallus gallus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
AUTHORS	1 (bases 1 to 1257)				
TITLE	Speltmann, F. and Brummendorf, T.				
JOURNAL	CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by developing cerebellar Purkinje cells				
MEDLINE	J. Neurosci. 16 (5), 1770-1779 (1996)				
REFERENCE	96370549				
AUTHORS	2 (bases 1 to 1257)				
TITLE	Brummendorf, T.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (17-MAY-1996) Brummendorf T., Max-Planck-Institute for Developmental Biology, Molecular Biology, Spemannstrasse 35, Tuebingen, Germany, 72076				
FEATURES	Location/Qualifiers				
source	1..1257				
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	/tissue_type="brain"				
	/clone_lib="lambda gt11"				
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	88..171				
	88..1149				
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	/evidence=experimental				
	/product="CEPU-1"				
	/protein_id="CAA96578.1"				
	/db_xref="GI:1325951"				
	/db_xref="SWISS-PROT:Q90773"				
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BASE COUNT	297 a	386 c	360 g	214 t	
ORIGIN					
Query Match	62.1%	Score 640.8;	DB 5;	Length 1257;	
Best Local Similarity	80.5%;	Pred. No. 4.7e-167;			
Matches 750;	Conservative	0;	Mismatches 182;	Indels 0;	Gaps 0;
QY	3	gaaaacatccagccaanaatgcacattctatctcttgygcaatcttcaaggygtgc	62		
Db	84	GAATATGGCCCGAGGAAATGAGACACCCGCTCATGGGTATCTTCGCCGGATGGC	143		
QY	63	tgtctgtgtctcttccaagagtgcccggtgcgcagcgagatgccaccttccccaaagc	122		
Db	144	CGCACTCCTCCTCTTCCAAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCAAGC	203		
QY	123	tatggacaacgctgacggtccgcgcaggggagagcgcacacctcaggtgcactattgacaa	182		
Db	204	TATGGACAACGCTGACTGTGCGGCAAGGGAGAGTGCCACGCTCAGGTGCTCGTGACAA	263		
QY	183	ccgggtcacccgggtggtgcctgctaaccgcagcaccatctctatgtgtggaatgacaa	242		
Db	264	CCGCGTCACCCCGTGGCTGGCTGAACCGCAGCAGCATCCTTATGCCGCAATGACAA	323		
QY	243	gtgtgtcctgatactctgcgctgtgtcctctgagcaacacccaacgcagctacatcgca	302		

Db	Accession	Gene	Species	Length	Source
Db	324	GTGGTGCCTTGGAGCCCGAGGGGTGGTGCCTCCTGGCCCAACACCCAAACCCAGTACAGCATCCA	383		
QY	303	gattccagaacgtgtgatgtgtatgaacagggcccttaccactgtctcgtgtgcagacagacaa	362		
Db	384	GATCCACGACGTGGACGCTGTACGATFAAGGGCCCTACACCTGCTCCGTGCAGACAGACAA	443		
QY	363	ccaccacaagaccctctaggggtccaccctcatctgtgtcaaglatctcccaaatlttagagat	422		
Db	444	TCACCCCAAGACATCTCGCGGTGCACCTCATTTGTGCAAGTGTCCGCCAAATATTACCGAGAC	503		
QY	423	ttcttcagatatctccatlaatgaagggacaatatatagcctcacctgcataagaaactg	482		
Db	504	CTCTTCTGACATCTTCATCATGAAGGTGGCAACGTTCAGCCTCACCTGCATAGCCACGGG	563		
QY	483	tagaacaagacctacggttacttctgagacacatctctccaaagcgttggcttlytag	542		
Db	564	CAGGCCAGACCCCAACATTCACCTGGAGACACATCTCGCCCAAGCTGTGGCTTCATCAG	623		
QY	543	tgaagacgaatacttggaaatlcaggagcatcacccggagcagtcagggtactacgagt	602		
Db	624	CGAGGACGAGTACCTGGAGATCACAGGCATCACGAGGAGAGCAGTGGCGAGTACGAGTG	683		
QY	603	cagtgcctccaatgacgttggccgcgcctgtgtacgagagatgaaggtacaccgtgaacta	662		
Db	684	CAGTGCCTCCACAGCAGCTGGCCGCGCTGTCTCAGCAGGAGTCAAAAGTCAACGTCAACTA	743		
QY	663	tcaccatacatcttcagaagccaaggttacaggtgtccccgttgggacaaagggacact	722		
Db	744	CCACACCGTACATTTCCGATGCGAAGACACCCGGTGTGCCGGTGGGGCAGAAAGGCATCCT	803		
QY	723	gcagtgtaagcctcagcagtcctccctcagcagaatccagtgtgtacaaggtacacaaag	782		
Db	804	GATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGTGTACAAAGACGACACGCG	863		
QY	783	actgattgaaggaagaaagggtgtgaaagtgtgaaacacagaccttcctcctcaaaactcat	842		
Db	864	GCTGCGCTGAAGGACAGCAAAAGGGCTGAAGGTGGAACCAAGCCTTCTCTCCCGACTGAC	923		
QY	843	ctctctcaatgtctctgtacacatgacatatygaactacacttgcgttgcctccaacaaagt	902		
Db	924	TTTCTTCAACGTTCTCGAGCAGGACTACGGCAACTACACCTGCTGTGGCTCCCAACGAGCT	983		
QY	903	gggcacacccaatgcccagcatcatgtctattg	934		
Db	984	AGGAACACCAACGCCAGCATGATCCTTATG	1015		
RESULT	6				
AB011810					
LOCUS	AB011810	1035 bp	mRNA	linear	VRT 09-JUL-1998
DEFINITION	Gallus gallus mRNA for CEPU-1, complete cds.				
ACCESSION	AB011810				
VERSION	AB011810.1	GI:3298455			
KEYWORDS	alternative splicing; CEPU-1.				
SOURCE	Gallus gallus CDNA to mRNA.				
ORGANISM	Gallus gallus				
REFERENCE					
AUTHORS	Kimura, Y., Shirabe, K. and Tanaka, H.				
TITLE	Submitted (03-MAR-1998) Yoshihige Kimura, Kumamoto University				
JOURNAL	Graduate School of Medical Sciences, Division of Developmental				
	Neurobiology; 4-24-1 Kuhnaji, Kumamoto, Kumamoto 862-0976, Japan				
	(E-mail: ykimura@gpo.kumamoto-u.ac.jp, Tel: 81-96-373-5294,				
	Fax: 81-96-373-5292)				
REFERENCE					
AUTHORS	Kimura, Y., Shirabe, K., Fukushima, M., Takeshita, M. and Tanaka, H.				
TITLE	CEPU-1: an immunoglobulin Superfamily Molecule, Has Cell Adhesion				
JOURNAL	Activity and Shows Dynamic Expression Patterns in Chick Embryonic				
	Spinal Cord				
	Unpublished (1998)				

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source		1..1035
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Best Local Similarity 79.3%; Pred. No. 1.1e-165;		
Matches 754; Conservative 0; Mismatches 197; Indels 0; Gaps 0;		
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Db	81	AGGAGTGCCCGGTGCGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAACAGTGA
QY	141	ccgcagcgagagagcgccacctcaagtgctactattgacaacgggtcacccggtgac 200
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QY	201	ctggctaaaccgcagcacctcctctatgtctggaatgacaagtgctgctgctctcg 260
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QY	261	cgtgctcctctgagcaacaccccaacgcagctacagcatcgagatccagaagctggt 320
Db	261	GGTGTGCTCTGGCCAAACCAAAACCAGTACAGCATCCAGATCCACGACGCTTGAC
QY	321	gtatgacgagggcccttaacctgtctcggtgcagacagacaacccaagaagctctag 380
Db	321	GTACGATGAAGGGCCCTACACCTGCTCCGTGCAGACAGACAAATCAACCCCAAG
QY	381	gtccacctcatgtgcaagtatcloccaaatgttagagatttctcagatatctccat 440
Db	381	CCTGACACTCATGTGCAAGTGTGCGCGAAATTAACCGAGATCTCTTGTGACATCT
QY	441	taatgaagggaacaatatattagccttaacctgcatagcaactggttagaccagaccta 500
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QY	501	tacttggaagacacatctctcccaaaagcgttggtcttgtgagtgaagacgaatactga 560
Db	501	CACCTGGAGACACATCTCGCCCAAGCTGTGGCTTCATCAGCGAGGAGGACGATAC
QY	561	aattcagggcatcacccgggagcagtcagggagtaagtgcaagtgctcctcaatgacgt 620
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QY	621	ggcgcgccccgtgtgtaagagaaagtgcaacgtgaactatccaccataattccaaga 680
Db	621	GGCGCGCCTGTGTCAGCGAGTCAAGTCAACCTCAACCTACCCACCTTACATCTCG
QY	681	agccaaggtacaggtgtcccgctgggacaaaaggagacactgcagtggtgaagcctcagc 740
Db	681	TGCGAAGAGCACCGGTGTGCGGGGGGCGAGAGGGGATCTGATGTGTGAAGCTCC
QY	741	agtcacctcagcagaattccagtggttacaagatgacaaaagactgattgaaggaagaa 800

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QY	801	agggtgaaagtgyaaacagaccttctctcaaaactcatcttctcaatgtctcga 860
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QY	921	catcatgctatttggtccagcgccgtcagcgaggtgagcaacgacgtcgagagggc 980
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RESULT	7	
AF271233		
LOCUS	1638 bp	DNA linear SYN 21-MAY-2001
DEFINITION	Synthetic construct secretory IgCEPUS-GFP fusion protein	
ACCESSION	AF271233	(IgCEPUS-GFP) gene, complete cds.
VERSION	AF271233.1	GI:14161268
KEYWORDS	synthetic construct.	
SOURCE	artificial sequence.	
ORGANISM	1 (bases 1 to 1638)	
REFERENCE	Kim,D.-S. and Moss,D.J.	
AUTHORS	Secretory IgCEPUS-GFP fusion protein expressions in transfected	
TITLE	cell lines	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1638)	
AUTHORS	Kim,D.-S. and Moss,D.J.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-MAY-2000) College of Natural Resources and Life	
	Science, Division of Biological Resources R-6517, Dong-A	
	University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of	
	Korea	

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CDS		
BASE COUNT		386 a 533 c 460 g 259 t
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Query Match 60.4%; Score 623.6; DB 12; Length 1638;		
Best Local Similarity 80.0%; Pred. No. 3e-162;		
Matches 734; Conservative 0; Mismatches 184; Indels 0; Gaps 0;		

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Db 6 CCAGGCGAAAAATGACGACACCCCGCTCTCATGGGTGATCTTCGCCGGATGGCCGCACTCCT 65
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QY 132 cgtgacggtccgacgagggagagcgccacctcaggtgacattatgacacccggtac 191
Db 126 CGTGAATGTGCGGCAAGGAGAGTGCCACGCTCAGGTGCTCCGTGACACACCGCGTCA 185
QY 192 ccggtggtcctggttaaacgcgacacccatctctatgtctggtgaatgacaaagtgtgct 251
Db 186 CCGGCTGGCCTGGGTGAACCGCACAGCATCTCTATGCCGCAATGACAGATGCTGCTT 245
QY 252 ggtatcctcgtgtgtctctcttgagcaacaccccaaacgcagttacagatcgagatccagaa 311
Db 246 GGACCCGAGGGGTGGTGTCTCTGCGCAACACCAAAACCCAGTACAGCATCCAGATCCACGA 305
QY 312 cgtgatatgtatgacgagggcccttacacctgctcgtgacagacagacaaaccccaaa 371
Db 306 CGTGAACGTGTACGATGAAGGGCCCTTACACCTGCTCCGTGCAGACAGACAAATCACCCCAA 365
QY 372 gacctctaggtgccacctcattgtgcaagtatcccaaaattgtagagattctctcaga 431
Db 366 GACATCTCGCGTGCACCTCATTTGTGCAAGTGTGCGCAAAATTACCAGATCTCTTCTGA 425
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QY 912 caatgcagcatcatgct 929
Db 906 GCCGGTGGCCACCATGCT 923

RESULT 8
AF292936 1013 bp mRNA linear VRT 24-AUG-2000
LOCUS AF292936
DEFINITION Gallus gallus CEPU-Se alpha 1 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292936
VERSION AF292936.1 GI:9887386
KEYWORDS

SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Lodge,A.P., McNamee,C.J., Howard,M.R., Reed,J.E. and Moss,D.J.
TITLE Characterisation of CEPU-Se, a secreted isoform of the IgLON family protein CEPU-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1013)
AUTHORS Lodge,A.P. and Moss,D.J.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The University of Liverpool, Ashton Street, Liverpool, Merseyside L69 3GE, UK

FEATURES
source location/Qualifiers
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BASE COUNT 230 a 309 c 293 g 181 t
ORIGIN

Query Match 58.6%; Score 604.8; DB 5; Length 1013;
Best Local Similarity 81.7%; Pred. No. 4.7e-157;
Matches 699; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 81 aggaagtgccctgctgcagcggagatgcccaccttcccaaaagtatgacaaagctgtgaagt 140
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Db 141 GCGGCAAGGGGAGAGTGCCACGCTCAGGTGCTCCGTGACAAACCGCGTCAACCCGCGTGGC 200
QY 201 ctggctaaccgcagcacacatcctctatgtggtgaatgacaaagtgtgctgacccctgcg 260
Db 201 CTGGCTGAACCGCAGACGATCCTCTATGGCGGCAATGACAAAGTGTGACCCGAG 260
QY 261 cgtggtcctctgagcaacacccaacgcagttacagcatcgatccagaacgtgtgattgt 320
Db 261 GGTGGTGTCTCTGGCCAAACCAAAACCCAGTACAGCATTCAGATCCACGACGTGACGT 320
QY 321 gtatgacgagggcccttacacctgctcgtgtgacagacaaacccaagaaccttag 380
Db 321 GTACGATGAAGGGCCCTTACACTGTCTCGTGCAGACAGACAAATCACCCCAAGACATCTCG 380
QY 381 ggtcacctcattgtgcaaatatccccaatgttagagattcttcagatatcccat 440
Db 381 CGTGACCTCATTTGTGCAAGTGTGCGCGAAATATACCGAGATCTCTTGACATCTCCAT 440
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QY	501	tacttgaagacacatctctccaaagcggttgcttctgtgagtgaagacgatacttga	560
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Db	561	GATCACAGGCATCAGCAGGAGCAGTGGGGCAGTACAGTGCATGCCCTCCACGACGT	620
QY	621	ggccgcgcccgtgtgaaggagagtaaaaggtcacccgtgaactatccacatacttcaaga	680
Db	621	GGCCGGCCCTGTCTGTCACGGAGTCAAGTCACCGTCAACTACCCACCGTACATCTGGA	680
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QY	801	agggtggaagtggaaaacacagaccttcctctcaaaactatcttccaatgtctctga	860
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DEFINITION	Gallus gallus mRNA for for OBCAM protein gamma isoform.		
ACCESSION	Y08170		
VERSION	Y08170.2	GI:4688845	
KEYWORDS	OBCAM protein.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
	Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 1533)		
AUTHORS	Wilson,D.J., Kim,D.S., Clarke,G.A., Marshall-Clarke,S. and Moss,D.J.		
TITLE	A family of glycoproteins (GP55), which inhibit neurite outgrowth, are members of the Ig superfamily and are related to OBCAM, neurotrimin, LAMP and CEPU-1		
JOURNAL	J. Cell. Sci. 109 (Pt 13), 3129-3138 (1996)		
MEDLINE	97157768		
REFERENCE	2 (bases 1 to 1533)		
AUTHORS	Lodge,A.P., Kim,D.S., Howard,M.R., McNamee,C.J., Smith,N. and Moss,D.J.		
TITLE	Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from chick: structural diversity of IgLON family proteins		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1533)		
AUTHORS	Wilson,D.J.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-MAR-1996) D.J.A. Wilson, Liverpool University, Human Anatomy and Cell Biology, Liverpool, L69 3BX, UK		
REMARK	Revised by [3]		
REFERENCE	4 (bases 1 to 1533)		
AUTHORS	Moss,D.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-1999) D.J. Moss, Liverpool University, Human Anatomy and Cell Biology, Liverpool, L69 3BX, UK		
COMMENT	On Apr 26, 1999 this sequence version replaced gi:1617043.		
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Query Match	54.9%;	Score 566.6;	DB 5;	Length 1533;
Best Local Similarity	72.5%;	Pred. NO. 2.1e-146;		
Matches 734; Conservative	0;	Mismatches 279;	Indels 0;	Gaps 0;

[illegible]

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RESULT	10
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LOCUS	AF292934
DEFINITION	Gallus gallus OBCAM alpha 1 isoform (OBCAM) mRNA, complete cds.
ACCESSION	AF292934
VERSION	AF292934.1 GI:9887382
KEYWORDS	.
SOURCE	chicken.
ORGANISM	Gallus gallus

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
TITLE	Phasianinae; Gallus.
JOURNAL	1 (bases 1 to 1556)
PUBMED	Lodge, A.P., Howard, M.R., McNamee, C.J. and Moss, D.J.
REFERENCE	Co-localisation, heterophilic interactions and regulated expression
AUTHORS	of IGLON family proteins in the chick nervous system
TITLE	Brain Res. Mol. Brain Res. 82 (1-2), 84-94 (2000)
JOURNAL	11042360
PUBMED	2 (bases 1 to 1556)
REFERENCE	Lodge, A.P. and Moss, D.J.
AUTHORS	Direct Submission
TITLE	Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The

FEATURES		3CE, UK	University of Liverpool, Ashton Street, Liverpool, Merseyside L69
source	Location/Qualifiers		
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CDS	17. .1051		

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Best Local Similarity		73.4%;	Pred. No. 5.1e-141;	Length 1556;

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QY	261	cgtgtctcttctg	agcaacaccccc	aacgcag	tacagcatc	gagatcc	agaac	gcgtg	atgt	320
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QY	321	gtatgcagagggcc	cttacaacctgtc	ggtgca	gacagacaac	ccccaag	acctctag			380
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QY 861 acatgactatyggaactaaccttgcgttgccctccaacaagctggycacaccatgccaag 920
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RESULT	11
BIOBCAM	
LOCUS	BIOBCAM
DEFINITION	Bovine mRNA for oploid binding protein/cell adhesion molecule
ACCESSION	U12672

VERSION X12672.1 GI:585
KEYWORDS cell adhesion molecule; glycoprotein; immunoglobulin superfamily;
membrane protein; opioid binding protein.
SOURCE
ORGANISM Bos taurus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 2593)
AUTHORS Schofield,P.R.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-1988) Schofield P.R
REFERENCE 2 (bases 1 to 2593)
AUTHORS Schofield,P.R., McFarland,K.C., Hayflick,J.S., Wilcox,J.N.,
Cho,T.M., Roy,S., Lee,N.M., Loh,H.H. and Seeburg,P.H.
TITLE Molecular characterization of a new immunoglobulin superfamily
protein with potential roles in opioid binding and cell contact
JOURNAL EMBO J. 8 (2), 489-495 (1989)
MEDLINE EMB0 J. 8 (2), 489-495 (1989)
COMMENT Data kindly reviewed (19-may-1989) by Schofield P.R.
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Best Local Similarity 73.6%; Pred. No. 3.8e-139;
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QY 261 cgtgtcctcttgagcaacaccacaacgcagttacagcatcgagatccagaacgtgaggt 320
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LOCUS RATCALMA 3069 bp mRNA linear ROD 08-MAY-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete CDS.
ACCESSION M88709
VERSION M88709.1 GI:203245
KEYWORDS cell adhesion-like molecule; opioid binding protein.
SOURCE Rattus norvegicus (strain Simonsen ICR) (library: UZ) brain cDNA to
mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3069)
AUTHORS Lippman,D.A., Lee,N.M. and Loh,H.H.
TITLE Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
rat brain cDNA library
JOURNAL Gene 117, 249-254 (1992)
MEDLINE 92347701
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RESULT 13
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LOCUS Human (clone PHOM) opioid-binding cell adhesion molecule mRNA, complete cds.
ACCESSION I34774.1 GI:514373
VERSION I34774.1
KEYWORDS opioid-binding cell adhesion molecule.
SOURCE Homo sapiens (library: Stratagene brain) occipital cortex cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1478)
AUTHORS Shark, K.B. and Lee, N.M.
TITLE Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a human opioid-binding cell adhesion molecule (OBAM)
JOURNAL Unpublished (1994)
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BASE COUNT 351 a 373 c 371 g 383 t
ORIGIN

Query Match 51.8%; Score 534.2; DB 9; Length 1478;
Best Local Similarity 73.2%; Pred. No. 2.1e-137;
Matches 699; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

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Db 191 CCGGCGAGGAGAGCGCCACCTCAGGTATACCATAGATGACCGGGTAAACCGGGTGGC 250
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 11, 2002, 22:58:27 ; Search time 66.43 Seconds

(without alignments)
126.485 Million cell updates/sec

Title: US-09-700-397-3
Perfect score: 1806
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	923.5	51.1	325	2	US-08-414-657D-41
5	923.5	51.1	338	2	US-08-414-657D-60
6	908	50.3	308	2	US-08-414-657D-46
7	907	50.2	315	2	US-08-414-657D-47
8	905	50.1	310	2	US-08-414-657D-45
9	902	49.9	304	2	US-08-414-657D-44
10	886.5	49.1	287	2	US-08-414-657D-48
11	885.5	49.0	287	2	US-08-414-657D-49
12	796.5	44.1	252	2	US-08-414-657D-56
13	795.5	44.0	252	2	US-08-414-657D-57
14	261	14.5	1395	4	US-09-540-245A-15
15	256	14.2	421	2	US-08-659-984A-1
16	256	14.2	421	4	US-08-660-531-1
17	256	14.2	444	4	US-08-659-984A-5
18	256	14.2	444	4	US-08-660-531-5
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22	246.5	13.6	1018	1	US-08-714-901-6
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25	243.5	13.5	1018	1	US-08-452-052-2
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27	237	13.1	73	2	US-08-414-657D-51

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30	229.5	12.7	869	1	US-08-374-834-16	Sequence 16, Appl
31	229.5	12.7	869	2	US-08-644-271-29	Sequence 29, Appl
32	225.5	12.5	478	5	PCT-US95-08493-15	Sequence 15, Appl
33	225.5	12.5	860	5	PCT-US95-08493-19	Sequence 19, Appl
34	225.5	12.5	868	5	PCT-US95-08493-21	Sequence 21, Appl
35	219	12.1	1091	3	US-08-986-485-5	Sequence 5, Appli
36	219	12.1	1101	3	US-08-986-485-2	Sequence 2, Appli
37	213	11.8	59	2	US-08-414-657D-52	Sequence 52, Appl
38	213	11.8	59	2	US-08-414-657D-53	Sequence 53, Appl
39	211	11.7	615	2	US-08-752-307B-9	Sequence 9, Appli
40	208.5	11.5	1651	4	US-09-540-245A-18	Sequence 18, Appl
41	205.5	11.4	596	2	US-08-752-307B-13	Sequence 13, Appl
42	201	11.1	946	5	PCT-US95-08493-13	Sequence 13, Appl
43	199	11.0	1241	4	US-09-040-774-2	Sequence 2, Appli
44	197.5	10.9	1447	4	US-09-041-886-25	Sequence 25, Appl
45	197.5	10.9	1447	5	PCT-US94-05277-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-42

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.18; Pred. No. 1.3e-84;

Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

```

QY 20 LAALCLF-QGVPRSGDATFPKAMNVTVRGEGSATLRCTIDNRVTRVAMLNRSITLYAG 78
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDPTALRCVVEDEKNSKVAMLNRSIGIIFAG 74

QY 79 NDKWCLDPRVLLSNQTQYSIEIQNDVYDEGPYTCVQFDNHPKTSRVHLIVQVSPKI 138
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 HDKWSLDPRVLEKRAHLEYSLRQKVDVYDEGSYTCVQTHPEPKTSQVYLIIVQVPPKI 134

QY 139 VEISSDISINEGNNISLTCTATGREPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 SNISSDYTVNEGSNVTLVCMANGREPVTITWRHLPLGREFEGEEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVYRKYVTNYPPIYISEAKGTGVVGQKGTLOCEASAVPSAEFQWYKD 258
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 195 YECKAANEVSSADVKQVKVTNYPPTITESKSNEATGROASLKEASAVPAPDFEWRD 254

QY 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHITNASIMLFGPGAVSE 318
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBEHYGNVTCVAANKLGVTNASLVLEFRPGSVRG 313

QY 319 VSNGTSRRAGCVWLLPLVLHLK 343
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 I-NGSISLAVPLWLLAASLFLCLSK 337
    
```

RESULT 2

```

US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-43
    
```

Query Match 51.3%; Score 926.5; DB 2; Length 338;
 Best Local Similarity 55.1%; Pred. No. 1.3e-84;
 Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

```

QY 20 LAALCLF-QGVPRSGDATFPKAMNVTVRGEGSATLRCTIDNRVTRVAMLNRSITLYAG 78
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDPTALRCVVEDEKNSKVAMLNRSIGIIFAG 74

QY 79 NDKWCLDPRVLLSNQTQYSIEIQNDVYDEGPYTCVQFDNHPKTSRVHLIVQVSPKI 138
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 HDKWSLDPRVLEKRAHLEYSLRQKVDVYDEGSYTCVQTHPEPKTSQVYLIIVQVPPKI 134

QY 139 VEISSDISINEGNNISLTCTATGREPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 SNISSDYTVNEGSNVTLVCMANGREPVTITWRHLPLGREFEGEEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVYRKYVTNYPPIYISEAKGTGVVGQKGTLOCEASAVPSAEFQWYKD 258
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 195 YECKAANEVSSADVKQVKVTNYPPTITESKSNEATGROASLKEASAVPAPDFEWRD 254

QY 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHITNASIMLFGPGAVSE 318
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBEHYGNVTCVAANKLGVTNASLVLEFRPGSVRG 313

QY 319 VSNGTSRRAGCVWLLPLVLHLK 343
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 I-NGSISLAVPLWLLAASLFLCLSK 337
    
```

RESULT 3

```

US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
    
```



```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-47
```

```
Query Match          50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 1e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;
```

```
QY 20 LAALCLF-QGVPRSGDATFRKAMDNVTVRGSESATLRCTIDNRVTRVAMLNRSITLYAG 78
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 17 LRLICLLPTGLPRVSD--FNKGTDNITVRGCDTAILRCVVEDKNSKVAMLNRSGITRAG 74

QY 79 NDKWCLDPRVVLISNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQSPKI 138
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 75 HDKWSLDPRVELKRAHLEYSLRIQKVVDYDEGSYTCVQTDQHEPKTSQVYLIQVPPKI 134

QY 139 VEISDISINEGNISLTCTATGRPEPTVWRHISPKAVGVSEDEYLEIQGITREGSD 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 135 SNISDVTVNEGSVTLVCMANGREPVITWRHLTPLGREFEGEEYLEILGITREGSGK 194

QY 199 YECASNDVAAPYVRKRVKVTNYPYISAKGTGVPVGOKGTLQCEASAVPSAEFQWTKD 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 195 YECKANEVSSADYKQVKVTNYPPTITESKSNKNEATGKQASLKCEASAVPAPDFEWYRD 254

QY 259 DKRLIEGKKGKVENRPLSKLIFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSE 318
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 255 DTR-INSANGLEIKSTEGSSLTVTNTEEHYGNITCVAAANKLGVTNASLVLFPGSVRG 313
```

```
QY 319 VS 320
:
Db 314 IN 315
```

```
RESULT 8
US-08-414-657D-45
; Sequence 45, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
```

```
;
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-45
```

```
Query Match          50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 1.6e-82;
Matches 173; Conservative 59; Mismatches 77; Indels 4; Gaps 3;
```

```
QY 31 VRSGDATFRKAMDNVTVRGSESATLRCTIDNRVTRVAMLNRSITLYAGNDKWCLDPRVYL 90
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 VRSDV--FNKGTDNITVRGCDTAILRCVVEDKNSKVAMLNRSGITRAGHDKWSLDPRVEL 58

QY 91 LSNITQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQSPKIYEISSDISINEG 150
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 59 EKRHALEYSLRIQKVVDYDEGSYTCVQTDQHEPKTSQVYLIQVPPKISNISDVTVNEG 118

QY 151 NNISLTCTATGRPEPTVWRHISPKAVGVSEDEYLEIQGITREGSDYECASANDVAAP 210
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 119 SNTLVCMANGREPVITWRHLTPLGREFEGEEYLEILGITREGSGKECKANEVSSA 178

QY 211 VVRKVTNYPYISAKGTGVPVGOKGTLQCEASAVPSAEFQWTKDKRLIEGKKGK 270
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 179 DVQYKVTNYPPTITESKSNKNEATGKQASLKCEASAVPAPDFEWYRDDTR-INSANGLE 237

QY 271 VNRNPLSKLIFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSEVSNGTSRACGV 330
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 238 IKSTEGSSLTVTNTEEHYGNITCVAAANKLGVTNASLVLFPGSVRGI-NGSISLAVPL 296

QY 331 WLPLVLHLHLK 343
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 297 WLHAASLFCILSK 309
```

```
RESULT 9
US-08-414-657D-44
; Sequence 44, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
```

```

; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-44
```

```

Query Match          49.9%; Score 902; DB 2; Length 304;
Best Local Similarity 55.5%; Pred. No. 3,1e-82;
Matches 171; Conservative 59; Mismatches 74; Indels 4; Gaps 3;
```

```

QY 31 VRSGDATEPKAMDNVTVRQGESATLRCITIDNRVTVAVMLNRSTILYAGNDKWCIDPRVVL 90
   ||| | | : ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 VRSVD--FNRGTDNITVRQGDALIRCVLEDKNSKVAVMLNRSGILFAGHDKWSLDPVEL 58

QY 91 LSNTOQYSIEIONVDVYDEGPYTCVSQTDNHPKTSRVHLIYOVSPIKIVEISSDISINEG 150
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 59 EKRHSLEYSLRIQKVVDYDEGSYTCVSQTOHEPKTSQVYLIYOVPKISNISSDVTNEG 118

QY 151 NNLSTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQGTRQSGDYECASNDVAAP 210
   :||| : ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 SNVTLCMANGRPEPTVTRHILPTGRFEFEGEELIILGITRQSGKYECKAANEVSSA 178

QY 211 VVRKVTYVNYPPYISAKGTGVPVGQKGTLCQCEASAVPSAEFQWKDKRLIEGKKGVK 270
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 179 DVQVKVTVNYPPYITTESKSNKNEATIGRQASLKEASAVPAPDFEWRDTR-INSANGLE 237

QY 271 VNRPFLEKLIFFNVSEHDYGNVTCVANSKLGHTNASIMLFGPGAVSEVSNISRRAGCV 330
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 238 IKSTEGQSSLTVTNVTTEHYGNVTCVAAANKLGVTNASLVLFRRGSVIRGI-NGSISLAVPL 296

QY 331 WLLPLVL 338
   ||| : |
Db 297 WLLAASL 304
```

```

RESULT 10
US-08-414-657D-48
; Sequence 48, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-48
```

```

Query Match          49.1%; Score 886.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 1e-80;
Matches 164; Conservative 57; Mismatches 66; Indels 3; Gaps 2;
```

```

QY 31 VRSGDATEPKAMDNVTVRQGESATLRCITIDNRVTVAVMLNRSTILYAGNDKWCIDPRVVL 90
   ||| | | : ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 VRSVD--FNRGTDNITVRQGDALIRCVLEDKNSKVAVMLNRSGILFAGHDKWSLDPVEL 58

QY 91 LSNTOQYSIEIONVDVYDEGPYTCVSQTDNHPKTSRVHLIYOVSPIKIVEISSDISINEG 150
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 59 EKRHSLEYSLRIQKVVDYDEGSYTCVSQTOHEPKTSQVYLIYOVPKISNISSDVTNEG 118

QY 151 NNLSTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQGTRQSGDYECASNDVAAP 210
   :||| : ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 SNVTLCMANGRPEPTVTRHILPTGRFEFEGEELIILGITRQSGKYECKAANEVSSA 178

QY 211 VVRKVTYVNYPPYISAKGTGVPVGQKGTLCQCEASAVPSAEFQWKDKRLIEGKKGVK 270
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 179 DVQVKVTVNYPPYITTESKSNKNEATIGRQASLKEASAVPAPDFEWRDTR-INSANGLE 237

QY 271 VNRPFLEKLIFFNVSEHDYGNVTCVANSKLGHTNASIMLFGPGAVSEVS 320
   :||| : ||| ||| ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| |||
Db 238 IKSTEGQSSLTVTNVTTEHYGNVTCVAAANKLGVTNASLVLFRRGSVIRGIN 287
```

```

RESULT 11
US-08-414-657D-49
; Sequence 49, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 287 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-414-657D-49

Query Match 49.0%; Score 885.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 1.3e-80;
Matches 164; Conservative 57; Mismatches 66; Indels 3; Gaps 2;

QY 31 VRSGDATPKAMDNVTVRQGESATLRCTIDNRVTRVAMLNKSTILYAGNDKWCLDPVYL 90
Db 1 VRSYD--FNRGTNITVRQGDALRCVVEDKNSKVAMLNRSGLIFAGHDKWSLDPVEL 58
QY 91 LSNQTQYSIEIONVDVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
Db 59 EKRALEYSLRQKVDVYDEGSYTCVQTDHPKTSQVLPKISNISSDVTVNEG 118
QY 151 NNISLTCIATGREPTVTWRHISPKAVGFSDEYLEIGITREOSGDYECASANDVAAP 210
Db 119 SNVTLVCMANGREPVITWRHLPLRGFEFGEHEYLEILGITREOSGKYECKAANEVSSA 178
QY 211 VVRKVTNVNPPYISEAKGTGVPVQKGTLOCEASAVPSAEFQWYKDKRLIEGKKGVK 270
Db 179 DVKQVKVTNPPYITTESKSNKATITGRQASLKEASAVPAPDFEWYRDTDR-INSANGLE 237
QY 271 VKNRPFLSKLIFNVSEHDYNTCVASNKLIGHTNASIMLFGPGAVSEVS 320
Db 238 IKSTEGQSSLTVTNVTTEHGYNTCVAAANKLGVTNASLVLEFRPGSVRGIN 287

RESULT 12
US-08-414-657D-56
; Sequence 56, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 252 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-414-657D-56

Query Match 44.1%; Score 796.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 8.5e-72;
Matches 144; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

QY 50 GESATLRCTIDNRVTRVAMLNKSTILYAGNDKWCLDPVYLLSNQTQYSIEIONVDYD 109
Db 1 GPVALRCVLEBDKNSKVAMLNRSGLIFAGHDKWSLDPVELKSHSLLEYSLRQKVDYD 60
QY 110 EGPYTCVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCIATGREPTVTW 169
Db 61 EGSYTCVQTDHPKTSQVLPKISNISSDVTVNEGSNVTLVCMANGREPEVITW 120
QY 170 RHISPKAVGFSDEYLEIGITREOSGDYECASANDVAAPVVRKVTNVNPPYISEAK 229
Db 121 RHILPTGREFEHEEYLEILGITREOSGKYECKAANEVSSADVQVKVTNPPYITESK 180
QY 230 GTGVPVQKGTLOCEASAVPSAEFQWYKDKRLIEGKKGVKNRPFSLKLIFFNVSEHD 289
Db 181 SNAATTGRQASLKEASAVPAPDFEWYRDTDR-INSANGLEIKSTEGQSSLTVTNVTTEH 239
QY 290 YGNVTCVASNKLK 302
Db 240 YGNVTCVAAANKLG 252

RESULT 13
US-08-414-657D-57
; Sequence 57, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-414-657D-57

Query Match          44.0%; Score 795.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 1.le-71;
Matches 144; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

QY 50 GBSATLRCTIDNRVTRVAVLNRSTILYAGNDKWCLEDPRVLLISNTQTQYSTIEIQNDVYD 109
   ||| ||| :::: ::||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GPTALRCVYEDKNSKVAWMLNRSGIIFAGHDKWSDLPVELERKHALLEYSLRIQKVDYD 60

QY 110 EGPYTCVQTDNHPKTSRYHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTW 169
   || ||||| : |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 EGSYTCVQIQHEPKTSQVYLLIVQVPEPKISNISSDVTYVNEGSNVTLVCMANGREPEVTW 120

QY 170 RHISPKAVGVSEDEYLEIQGITRESGDYEGCSASNDYAAPVYRKYVTYVPPYISEAK 229
   ||::|| | |::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 RHLPLRGREFEGEEYLEILGITREOSGKYECKAANEVSSADYQVKYVYVNPPTITESH 180

QY 230 GTGVPVYGQKGLQCEASAVPSAEFQWYKDDKRLLEGKKGVKENRPFSLKLIFFNVSEHD 289
   ||:: ::||| ||| ::||| ||| | | |::: || | | ||| |||
Db 181 SNEATTGRQASLKCFAASAVPAPDFEWYRDDTR-INSANGLEIKSTEGOSSLTVTNVTSH 239

QY 290 YGNVTCVASNKLK 302
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Db 240 YGNVTCVAAANKLG 252

RESULT 14
US-09-540-245A-15
; Sequence 15, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A

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; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/0065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1395
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-540-245A-15

Query Match          14.5%; Score 261; DB 4; Length 1395;
Best Local Similarity 26.1%; Pred. No. 5.7e-17;
Matches 80; Conservative 49; Mismatches 127; Indels 50; Gaps 9;

QY 38 FPRAMDNVTVRGSESATLRCTI-DNRVTRVAV-----LNRSTILYAGNDKWCIDPRV 88
   | | : : |::| |:: : : | | :::| |:
Db 257 FMKEPKDQVMLYGQATFHCYSVGDPDPKVLWKKEGNIPVSRARILH----- 304
   : |::| |: |::| |: :::| | | | : : |:

QY 89 VLLSNTQTQYSIEIQNDVYDEGPYTCVSQTDNHPKTSRVHLIVQVSPKIVEISSDISIN 148
   : |::| |: |::| |: :::| | | | : : |:
Db 305 -----DEKSLSEISNITPTDEGTVCCEAHNNVGQISARASLIYVAPNFTKRPSNKKVG 357
   : |::| |: |::| |: :::| | | | : : |:

QY 149 EGNNTSLTCIATGPEPTVTRHITSPKAVG-----VSEDEYLEIQGITREQSGDY 199
   : |::| |: |::| |: :::| | | | : : |:
Db 358 LNVGVQLPCMASGNPPSVFMTKEGVSTLMPNNSHGROYAADGILQITDVRQEDEGY 417
   : |::| |: |::| |: :::| | | | : : |:

QY 200 ECGASNDVAPVVR--RVKVTVWVP--YISEAKGITGVPVGQKGTLCCEASAVPSAEF 253
   ||: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |:
Db 418 VCSAFSVVDSSIVRVFLQVSSVDERPPPIIQIGPANQT-LPKGSVATLPCRATGNPSPRI 476
   : |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |:

QY 254 QWYKDDKRLIEGKKGVKVENRPFISKLIFFNVSEHDYGNITCVASNKLGHTN--ASIMLF 311
   : |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |:
Db 477 KWFHGHAVQAGNRYSIIQG---SLRVDDLQLSDSGTYTCTASGERGETSWAATLVE 532
   : |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |:

QY 312 GPGAVS 317
   ||: |
Db 533 KPGSTS 538

RESULT 15
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2002, 00:25:57 ; Search time 277.62 Seconds

(without alignments)
436.140 Million cell updates/sec

Title: US-09-700-397-3

Perfect score: 1806
Sequence: 1 MKTIQPKMHSISWAIPTGL.....RRAGCVLLPLVHLHLKE 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	344	17	US-09-380-138-523
2	1806	100.0	344	21	US-09-700-397-3
3	1806	100.0	344	23	US-09-918-585A-523
4	1806	100.0	344	23	US-09-978-188A-523
5	1806	100.0	344	23	US-09-978-189-523
6	1806	100.0	344	23	US-09-978-191A-523
7	1806	100.0	344	23	US-09-978-192-523

8	1806	100.0	344	23	US-09-978-192A-523	Sequence 523, App
9	1806	100.0	344	23	US-09-978-193A-523	Sequence 523, App
10	1806	100.0	344	23	US-09-978-194A-523	Sequence 523, App
11	1806	100.0	344	23	US-09-978-295A-523	Sequence 523, App
12	1806	100.0	344	23	US-09-978-298A-523	Sequence 523, App
13	1806	100.0	344	23	US-09-978-299A-523	Sequence 523, App
14	1806	100.0	344	23	US-09-978-585-523	Sequence 523, App
15	1806	100.0	344	23	US-09-978-585A-523	Sequence 523, App
16	1806	100.0	344	23	US-09-978-608-523	Sequence 523, App
17	1806	100.0	344	23	US-09-978-608A-523	Sequence 523, App
18	1806	100.0	344	23	US-09-978-643-523	Sequence 523, App
19	1806	100.0	344	23	US-09-978-643A-523	Sequence 523, App
20	1806	100.0	344	23	US-09-978-665A-523	Sequence 523, App
21	1806	100.0	344	23	US-09-978-697-523	Sequence 523, App
22	1806	100.0	344	23	US-09-978-802A-523	Sequence 523, App
23	1806	100.0	344	23	US-09-978-824-523	Sequence 523, App
24	1806	100.0	344	23	US-09-981-915A-523	Sequence 523, App
25	1806	100.0	344	23	US-09-999-830A-523	Sequence 523, App
26	1806	100.0	344	23	US-09-999-832A-523	Sequence 523, App
27	1806	100.0	344	23	US-09-999-833A-523	Sequence 523, App
28	1806	100.0	344	23	US-09-999-834A-523	Sequence 523, App
29	1806	100.0	344	24	US-10-002-796-104	Sequence 104, App
30	1806	100.0	344	24	US-10-002-967A-523	Sequence 523, App
31	1806	100.0	344	24	US-10-013-922A-523	Sequence 523, App
32	1806	100.0	344	24	US-10-017-191A-523	Sequence 523, App
33	1806	100.0	344	24	US-10-020-445A-523	Sequence 376, App
34	1806	100.0	344	24	US-10-028-072-376	Sequence 104, App
35	1806	100.0	344	24	US-10-066-193-104	Sequence 104, App
36	1806	100.0	344	24	US-10-066-198-104	Sequence 104, App
37	1806	100.0	344	24	US-10-066-203-104	Sequence 104, App
38	1806	100.0	344	24	US-10-066-211-104	Sequence 104, App
39	1806	100.0	344	24	US-10-066-269-104	Sequence 104, App
40	1806	100.0	344	24	US-10-066-273-104	Sequence 104, App
41	1806	100.0	344	24	US-10-066-494-104	Sequence 104, App
42	1806	100.0	344	24	US-10-066-500-104	Sequence 56, Appl
43	1806	100.0	344	24	US-10-081-056-56	Sequence 5430, Ap
44	1806	100.0	355	18	US-09-488-725A-5430	Sequence 4, Appli
45	1799	99.6	344	19	US-09-544-511-4	

ALIGNMENTS

RESULT 1
US-09-380-138-523
; Sequence 523, Application US/09380138
; GENERAL INFORMATION:
; APPLICANT: Wood, William I.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Yuan, Jean
; APPLICANT: Baker, Kevin P.
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2630RLE
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US/09/380,138
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: US 60/077,450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/077,632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: US 60/077,791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: US 60/078,004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 60/078,886


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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/086,430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 60/087,208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,038
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 538
; SEQ ID NO 523
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-380-138-523
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Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKTIQPKMNSISWAIFTGLALCLFQGVPRSGDATEPKAMDNTVRQGESATLRCTID 60
QY 61 NRYTRVAMLNRSITLYAGNDKWCLDPRVLLSNQTQYSIEIQNVYVDEGPTCSVQTD 120
    |||||||
Db 61 NRYTRVAMLNRSITLYAGNDKWCLDPRVLLSNQTQYSIEIQNVYVDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
    |||||||
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQITRQSGDYECASNDVAAPVRRVKTVMNPPYISEAKGTGVPVQOKGT 240
    |||||||
Db 181 SEDEYLEIQITRQSGDYECASNDVAAPVRRVKTVMNPPYISEAKGTGVPVQOKGT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKENRPLSKLIFENVSEHDYGNNTCVASNK 300
    |||||||
Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKENRPLSKLIFENVSEHDYGNNTCVASNK 300
QY 301 LGHTNASIMLFGPAVSEVSNGTSSRAGCWWLLPLVLHLLKF 344
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Db 301 LGHTNASIMLFGPAVSEVSNGTSSRAGCWWLLPLVLHLLKF 344
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RESULT 2
US-09-700-397-3
; Sequence 3, Application US/09700397
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Novel Polypeptides, cDNA encoding the same, and use of them
; FILE REFERENCE: 061459
; CURRENT APPLICATION NUMBER: US/09/700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Clone OC001 derived from human brain
; US-09-700-397-3
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Query Match 100.0%; Score 1806; DB 21; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKTIQPKMNSISWAIFTGLALCLFQGVPRSGDATEPKAMDNTVRQGESATLRCTID 60
QY 61 NRYTRVAMLNRSITLYAGNDKWCLDPRVLLSNQTQYSIEIQNVYVDEGPTCSVQTD 120
    |||||||
Db 61 NRYTRVAMLNRSITLYAGNDKWCLDPRVLLSNQTQYSIEIQNVYVDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
    |||||||
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQITRQSGDYECASNDVAAPVRRVKTVMNPPYISEAKGTGVPVQOKGT 240
    |||||||
Db 181 SEDEYLEIQITRQSGDYECASNDVAAPVRRVKTVMNPPYISEAKGTGVPVQOKGT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKENRPLSKLIFENVSEHDYGNNTCVASNK 300
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Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKENRPLSKLIFENVSEHDYGNNTCVASNK 300
QY 301 LGHTNASIMLFGPAVSEVSNGTSSRAGCWWLLPLVLHLLKF 344
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Db 301 LGHTNASIMLFGPAVSEVSNGTSSRAGCWWLLPLVLHLLKF 344
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RESULT 3
US-09-918-585A-523
; Sequence 523, Application US/09918585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817

1	PRIOR FILING DATE: 1998-04-15
2	PRIOR APPLICATION NUMBER: 60/081819
3	PRIOR FILING DATE: 1998-04-15
4	PRIOR APPLICATION NUMBER: 60/081952
5	PRIOR FILING DATE: 1998-04-15
6	PRIOR APPLICATION NUMBER: 60/081838
7	PRIOR FILING DATE: 1998-04-15
8	PRIOR APPLICATION NUMBER: 60/082568
9	PRIOR FILING DATE: 1998-04-21
10	PRIOR APPLICATION NUMBER: 60/082569
11	PRIOR FILING DATE: 1998-04-21
12	PRIOR APPLICATION NUMBER: 60/082704
13	PRIOR FILING DATE: 1998-04-22
14	PRIOR APPLICATION NUMBER: 60/082804
15	PRIOR FILING DATE: 1998-04-22
16	PRIOR APPLICATION NUMBER: 60/082700
17	PRIOR FILING DATE: 1998-04-22
18	PRIOR APPLICATION NUMBER: 60/082797
19	PRIOR FILING DATE: 1998-04-22
20	PRIOR APPLICATION NUMBER: 60/082796
21	PRIOR FILING DATE: 1998-04-23
22	PRIOR APPLICATION NUMBER: 60/083336
23	PRIOR FILING DATE: 1998-04-27
24	PRIOR APPLICATION NUMBER: 60/083322
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26	PRIOR APPLICATION NUMBER: 60/083392
27	PRIOR FILING DATE: 1998-04-29
28	PRIOR APPLICATION NUMBER: 60/083495
29	PRIOR FILING DATE: 1998-04-29
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31	PRIOR FILING DATE: 1998-04-29
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33	PRIOR FILING DATE: 1998-04-29
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40	PRIOR APPLICATION NUMBER: 60/083559
41	PRIOR FILING DATE: 1998-04-29
42	PRIOR APPLICATION NUMBER: 60/083500
43	PRIOR FILING DATE: 1998-04-29
44	PRIOR APPLICATION NUMBER: 60/083742
45	PRIOR FILING DATE: 1998-04-30
46	PRIOR APPLICATION NUMBER: 60/084366
47	PRIOR FILING DATE: 1998-05-05
48	PRIOR APPLICATION NUMBER: 60/084414
49	PRIOR FILING DATE: 1998-05-06
50	PRIOR APPLICATION NUMBER: 60/084441
51	PRIOR FILING DATE: 1998-05-06
52	PRIOR APPLICATION NUMBER: 60/084637
53	PRIOR FILING DATE: 1998-05-07
54	PRIOR APPLICATION NUMBER: 60/084639
55	PRIOR FILING DATE: 1998-05-07
56	PRIOR APPLICATION NUMBER: 60/084640
57	PRIOR FILING DATE: 1998-05-07
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59	PRIOR FILING DATE: 1998-05-07
60	PRIOR APPLICATION NUMBER: 60/084600
61	PRIOR FILING DATE: 1998-05-07
62	PRIOR APPLICATION NUMBER: 60/084627
63	PRIOR FILING DATE: 1998-05-07
64	PRIOR APPLICATION NUMBER: 60/084643
65	PRIOR FILING DATE: 1998-05-07
66	PRIOR APPLICATION NUMBER: 60/085339
67	PRIOR FILING DATE: 1998-05-13
68	PRIOR APPLICATION NUMBER: 60/085338
69	PRIOR FILING DATE: 1998-05-13
70	PRIOR APPLICATION NUMBER: 60/085323
71	PRIOR FILING DATE: 1998-05-13
72	PRIOR APPLICATION NUMBER: 60/085582
73	PRIOR FILING DATE: 1998-05-15

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; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18

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Query Match          100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
Db 61 NRVTRVAMLRSTILVAGNDKWCIDBRVLLSNTOQYSIEIQNVYVDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTRHISKAVGFV 180
    |||||||
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTRHISKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECASANDVAAPVRRVAVTVNPPYISEAKGTGVYVQOKGT 240
    |||||||
Db 181 SEDEYLEIQGITREQSGDYECASANDVAAPVRRVAVTVNPPYISEAKGTGVYVQOKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPLSKLIFENVSEHDYGNATCVASNK 300
    |||||||
Db 241 LOCEASAVPSAEFQWKDKRLIEGKGVKVENRPLSKLIFENVSEHDYGNATCVASNK 300
QY 301 LGHTNASIMLFGPAGVSEVNGTSRRAGCWWLLPLVLHLLKKE 344
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Db 301 LGHTNASIMLFGPAGVSEVNGTSRRAGCWWLLPLVLHLLKKE 344

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RESULT 4
US-09-978-188A-523
; Sequence 523, Application US/09978188A
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

```

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC8
; CURRENT APPLICATION NUMBER: US/09/978.188A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-04-01

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; PRIOR APPLICATION NUMBER: 60/081070
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMNSISWAIFTGLALCLFQGVVPRSGDATFPKAMDNVTVRQGESATIRCTID 60
DB 1 MKTIQPKMNSISWAIFTGLALCLFQGVVPRSGDATFPKAMDNVTVRQGESATIRCTID 60
QY 61 NRYTRVAMLNKSTILYAGNDKWCCLDPVYLLSNTQTOYSIEIQNVYVDEGPYTCYQTD 120
DB 61 NRYTRVAMLNKSTILYAGNDKWCCLDPVYLLSNTQTOYSIEIQNVYVDEGPYTCYQTD 120
QY 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFV 180
DB 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQGTREQSGDYECASANDVAAPVVRKVTVNPPIYISEAKGTGVPVQKGT 240
DB 181 SEDEYLEIQGTREQSGDYECASANDVAAPVVRKVTVNPPIYISEAKGTGVPVQKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKKGVVENRPFISKLIFFNVSCHDYGNITYVASNK 300
DB 241 LOCEASAVPSAEFQWKDKRLIEGKKGVVENRPFISKLIFFNVSCHDYGNITYVASNK 300
QY 301 LGHTNASIMLFGPAGVSEVNGTSRRAGCWWLLPLVHLHLKF 344
DB 301 LGHTNASIMLFGPAGVSEVNGTSRRAGCWWLLPLVHLHLKF 344

RESULT 5
US-09-978-189-523
; Sequence 523, Application US/09978189
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.3e-163;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MKTIQPKMHSISWAIFTGLALCLTQGVPPVRSQDAPPKAMDNVTVRQGESATLRCTID 60
 QY 61 NRVTAVAMLRSTILYAGNDKWLDPVYLLSNTQTYXSEIQNVVYDEGPYTCVQTD 120
 Db 61 NRVTAVAMLRSTILYAGNDKWLDPVYLLSNTQTYXSEIQNVVYDEGPYTCVQTD 120
 QY 121 NHPKTSRVHLIVQVSPKVEISSDISINEGNNISLTICATGRPEPTVTVRHRISKAVGFV 180
 Db 121 NHPKTSRVHLIVQVSPKVEISSDISINEGNNISLTICATGRPEPTVTVRHRISKAVGFV 180
 QY 181 SEDEYLEIGITRQSGDYECSASNDVAAAPVRRVYKVTVNPPIYSEAKGTGVPVGQKGT 240

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|||||
Db 181 SEDEYLEIGITRESGDYECASNDVAAPVVRVKVTNVPYISEAKGVPVGQGT 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPLSKLIEFNVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPLSKLIEFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNSTSRKAGCVMILPLVLHLILKE 344
Db 301 LGHTNASIMLFGPGAVSEVSNSTSRKAGCVMILPLVLHLILKE 344

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RESULT 7

US-09-978-192-523

; Sequence 523, Application US/09978192

; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 NRVTRVAMLNRSITLYAGNDKWCLDPVYLLSNTOQYSIEIONVDYDEGPYTCVSQTD 120
Db 61 NRVTRVAMLNRSITLYAGNDKWCLDPVYLLSNTOQYSIEIONVDYDEGPYTCVSQTD 120
QY 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLFCIATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLFCIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECASNDVAAPVYRRVKYTVNYPPIYSEAKGTGVPVQOKGT 240
Db 181 SEDEYLEIQGITREQSGDYECASNDVAAPVYRRVKYTVNYPPIYSEAKGTGVPVQOKGT 240
QY 241 LQCEASAVPSAEFQWYKDKRLIEGKKGVKENRPELSKLIFFNVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWYKDKRLIEGKKGVKENRPELSKLIFFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPQAVSEVSNGTSRAGCWLLPLVHLLKLF 344
Db 301 LGHTNASIMLFGPQAVSEVSNGTSRAGCWLLPLVHLLKLF 344

RESULT 8
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; Sequence 523, Application US/09978192A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavira, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1,3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMNSISWATFTGLALCLFQGVPRVRSQDATFPKAMDNTVROGESATLRCCTID 60
Db 1 MKTIQPKMNSISWATFTGLALCLFQGVPRVRSQDATFPKAMDNTVROGESATLRCCTID 60
QY 61 NRVTRVAMLNRSITILYAGNDKWCLDPRVLLSNTQTOYSIEIQNDVYDEGPTCSVQTD 120
Db 61 NRVTRVAMLNRSITILYAGNDKWCLDPRVLLSNTQTOYSIEIQNDVYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISKAVGFV 180
QY 181 SEDEYLEIOGITREOSGDYECSSANDYAAPVVRKRVTVNYPPIYSEAKGTGVPVQOKGT 240
Db 181 SEDEYLEIOGITREOSGDYECSSANDYAAPVVRKRVTVNYPPIYSEAKGTGVPVQOKGT 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKENRPELSKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKENRPELSKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCWLLPLLYLHLLKE 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCWLLPLLYLHLLKE 344

RESULT 9

US-09-978-193A-523
; Sequence 523, Application US/09978193A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC6
; CURRENT APPLICATION NUMBER: US/09/978,193A

;; CURRENT FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNSTSWAIFTGLAALCLFQGVPRVSGDATFPKAMDNTVRGSESATLRCTID 60
Db 1 MKTIQPKMHNSTSWAIFTGLAALCLFQGVPRVSGDATFPKAMDNTVRGSESATLRCTID 60
QY 61 NRYTRVAMLNRSITLLYAGNDKWCIDPRVLLSNTQTQYSTIETIQNVDYDEGPTCSVQTD 120
Db 61 NRYTRVAMLNRSITLLYAGNDKWCIDPRVLLSNTQTQYSTIETIQNVDYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGTRQSGDYECSASNDVAAPVVRVKVTVNPYPYISEAKGTGVPVGOKGT 240
Db 181 SEDEYLEIQGTRQSGDYECSASNDVAAPVVRVKVTVNPYPYISEAKGTGVPVGOKGT 240
QY 241 LQCEASAVPSAEFQWKDKDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDKDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPAVSEVSNSTSRRACGCVLLPLVLHLHLKE 344
Db 301 LGHTNASIMLFGPAVSEVSNSTSRRACGCVLLPLVLHLHLKE 344

RESULT 10
US-09-978-194A-523
; Sequence 523, Application US/09978194A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C10
CURRENT APPLICATION NUMBER: US/09/978,194A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15

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Query Match      100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      1  MKTIQPKMNSISWALFTGLALCLFQGVPRSGDATEPKAMNVTVRQGESATLRCITD 60
Db      1  MKTIQPKMNSISWALFTGLALCLFQGVPRSGDATEPKAMNVTVRQGESATLRCITD 60
QY      61  NRVTRAWLNRSTILYAGNDKWCLEPRVLLSNTQTOYSIEIONVDYDEGPTCSVQTD 120
      61  NRVTRAWLNRSTILYAGNDKWCLEPRVLLSNTQTOYSIEIONVDYDEGPTCSVQTD 120
Db      61  NRVTRAWLNRSTILYAGNDKWCLEPRVLLSNTQTOYSIEIONVDYDEGPTCSVQTD 120
QY      121  NHPKTSRYHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
      121  NHPKTSRYHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
Db      121  NHPKTSRYHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
QY      181  SEDEYLEIQTREQSGDYECASASNDVAAPVVRKVTVNYPPYISEAKGTGVPVGQKGT 240
      181  SEDEYLEIQTREQSGDYECASASNDVAAPVVRKVTVNYPPYISEAKGTGVPVGQKGT 240
Db      181  SEDEYLEIQTREQSGDYECASASNDVAAPVVRKVTVNYPPYISEAKGTGVPVGQKGT 240
QY      241  LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
      241  LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db      241  LQCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
QY      301  LGHTNASIMLFGPAGAVSEVSNSTRRAGCWLPLVLHLLKPF 344
      301  LGHTNASIMLFGPAGAVSEVSNSTRRAGCWLPLVLHLLKPF 344
Db      301  LGHTNASIMLFGPAGAVSEVSNSTRRAGCWLPLVLHLLKPF 344

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RESULT 11
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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan

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; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATFPKAMDNTVROGESATLRCTID 60
Db 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATFPKAMDNTVROGESATLRCTID 60
QY 61 NRYTRVAVLNKSTILLYAGNDKWCLDPRVVLISNTQTQYSIEIQNVVDYDEGPYTCVQTD 120
Db 61 NRYTRVAVLNKSTILLYAGNDKWCLDPRVVLISNTQTQYSIEIQNVVDYDEGPYTCVQTD 120
QY 121 NHPKTSRVHLIYQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIYQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEVLEIQTREQSGDYECSSANDVAAPVRYRVKVTVNPPIYSEAKGTGVPVGQKT 240
Db 181 SEDEVLEIQTREQSGDYECSSANDVAAPVRYRVKVTVNPPIYSEAKGTGVPVGQKT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGVYENRPFLSKLIFNVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGVYENRPFLSKLIFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLEFGPAVSEVSNGTSSRRAGCVLLPLVLHLILKE 344

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Db 301 LGHTNASIMLFPGAVSEVSNSTSRAGCVMLPLVLHLIKF 344
RESULT 12
US-09-978-298A-523
; Sequence 523, Application US/09978298A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC2
; CURRENT APPLICATION NUMBER: US/09/978,298A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/080194
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; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083495
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLALCLFQGVPRVSGDATEPKAMDNTVROGESATLRCTID 60
Db 1 MKTIQPKMHNISWAIFTGLALCLFQGVPRVSGDATEPKAMDNTVROGESATLRCTID 60
QY 61 NRVTRVAMLNRSITLYAGNDKWCIDPRVVLISNTQTQYSIEIQNVDDYDEGPTYCSVQTD 120
Db 61 NRVTRVAMLNRSITLYAGNDKWCIDPRVVLISNTQTQYSIEIQNVDDYDEGPTYCSVQTD 120

QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQITREQSGDYECGSASNDVAPVRRVKVTVNYPPISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQITREQSGDYECGSASNDVAPVRRVKVTVNYPPISEAKGTGVPVGQKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKKGAVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEFQWKDKRLIEGKKGAVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLPFGAVSEVSNGTSRRAGCVWLLPLVLHLLKF 344
Db 301 LGHTNASIMLPFGAVSEVSNGTSRRAGCVWLLPLVLHLLKF 344

RESULT 13
US-09-978-299A-523
; Sequence 523, Application US/09978299A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C3
; CURRENT APPLICATION NUMBER: US/09/978, 299A
; PRIOR APPLICATION NUMBER: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12


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Query Match          100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKMHNISWAIIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
QY 61 NRYTRVAMLNRSTILLYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDYDEGPTYCSVQTD 120
Db 61 NRYTRVAMLNRSTILLYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDYDEGPTYCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECSSASNDVAAPYRRVKVTYVNPYPISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQGITREQSGDYECSSASNDVAAPYRRVKVTYVNPYPISEAKGTGVPVGQKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWWLLPLVLHLLIKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWWLLPLVLHLLIKF 344

RESULT 14
US-09-978-585-523
; Sequence 523, Application US/09978585
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 523
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585-523
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Query Match          100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKMHNISWAIIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
QY 61 NRYTRVAMLNRSTILLYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDYDEGPTYCSVQTD 120
Db 61 NRYTRVAMLNRSTILLYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDYDEGPTYCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECSSASNDVAAPYRRVKVTYVNPYPISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQGITREQSGDYECSSASNDVAAPYRRVKVTYVNPYPISEAKGTGVPVGQKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWWLLPLVLHLLIKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWWLLPLVLHLLIKF 344

RESULT 15
US-09-978-585A-523
; Sequence 523, Application US/09978585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 523
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-978-585A-523

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCCTID 60
|||||
Db 1 MKTIQPKMHNISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCCTID 60
QY 61 NRYTRVAVLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIONVDVYDEGPTCSVQTD 120
|||||
Db 61 NRYTRVAVLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIONVDVYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLTCTATGRPEPTVYWRHISPKAVGFV 180
|||||
Db 121 NHPKTSRVHLIVQVSPKIYEISSDISINEGNNISLTCTATGRPEPTVYWRHISPKAVGFV 180
QY 181 SEDEYLEIQTITREQSGDYECASASNDVAAPVYRRVKYTVNYPPIYISAKGTGVPYGOKGT 240
|||||
Db 181 SEDEYLEIQTITREQSGDYECASASNDVAAPVYRRVKYTVNYPPIYISAKGTGVPYGOKGT 240
QY 241 LOCEASAVPSAEFQWYKDDKRLIEGKKGVYVENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
|||||
Db 241 LOCEASAVPSAEFQWYKDDKRLIEGKKGVYVENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWLLPLLVHLLKF 344
|||||
Db 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCWLLPLLVHLLKF 344

Search completed: July 12, 2002, 00:41:09
Job time: 912 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 12, 2002, 00:33:02 ; Search time 73.58 Seconds

(without alignments)
485.542 Million cell updates/sec

Title: US-09-700-397-3

Perfect score: 1806
Sequence: 1 MKTIQPKMHSISWAIPTGL.....RRAGCWLPLVLHLLEKF 344Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 323636 seqs, 103855142 residues

Total number of hits satisfying chosen parameters: 323636

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1806	100.0	344	5	US-09-978-403A-523 Sequence 523, App
2	1806	100.0	344	5	US-09-978-544A-523 Sequence 523, App
3	1806	100.0	344	5	US-09-978-681A-523 Sequence 523, App
4	1806	100.0	344	5	US-09-978-757A-523 Sequence 523, App
5	1806	100.0	344	5	US-09-978-564A-523 Sequence 523, App
6	1806	100.0	344	5	US-09-999-831A-523 Sequence 523, App
7	1806	100.0	344	5	US-09-999-829A-523 Sequence 523, App
8	1806	100.0	344	5	US-09-978-375A-523 Sequence 523, App
9	1806	100.0	344	5	US-09-978-423A-523 Sequence 523, App
10	1806	100.0	344	6	US-10-013-921A-523 Sequence 523, App
11	1806	100.0	344	6	US-10-013-929A-523 Sequence 523, App
12	1806	100.0	344	6	US-10-013-918A-523 Sequence 523, App
13	1806	100.0	344	6	US-10-017-082A-523 Sequence 523, App
14	1806	100.0	344	6	US-10-119-480-126 Sequence 126, App
15	1806	100.0	344	6	US-10-121-049-376 Sequence 376, App
16	1806	100.0	344	6	US-10-121-050-376 Sequence 376, App
17	1806	100.0	344	6	US-10-121-053-376 Sequence 376, App
18	1806	100.0	344	6	US-10-121-043-376 Sequence 376, App
19	1806	100.0	344	6	US-10-121-044-376 Sequence 376, App
20	1806	100.0	344	6	US-10-121-054-376 Sequence 376, App
21	1806	100.0	344	6	US-10-121-056-376 Sequence 376, App
22	1806	100.0	344	6	US-10-121-057-376 Sequence 376, App
23	1806	100.0	344	6	US-10-121-058-376 Sequence 376, App
24	1806	100.0	344	6	US-10-121-060-376 Sequence 376, App
25	1806	100.0	344	6	US-10-121-063-376 Sequence 376, App
26	1806	100.0	344	6	US-10-121-063-376 Sequence 376, App

27	1806	100.0	344	6	US-10-123-108-376 Sequence 376, App
28	1806	100.0	344	6	US-10-123-154-376 Sequence 376, App
29	1806	100.0	344	6	US-10-123-156-376 Sequence 376, App
30	1806	100.0	344	6	US-10-123-157-376 Sequence 376, App
31	1806	100.0	344	6	US-10-123-212-376 Sequence 376, App
32	1806	100.0	344	6	US-10-123-213-376 Sequence 376, App
33	1806	100.0	344	6	US-10-123-109-376 Sequence 376, App
34	1806	100.0	344	6	US-10-121-041-376 Sequence 376, App
35	1806	100.0	344	6	US-10-121-045-376 Sequence 376, App
36	1806	100.0	344	6	US-10-121-046-376 Sequence 376, App
37	1806	100.0	344	6	US-10-121-051-376 Sequence 376, App
38	1806	100.0	344	6	US-10-121-048-376 Sequence 376, App
39	1806	100.0	344	6	US-10-121-052-376 Sequence 376, App
40	1806	100.0	344	6	US-10-121-061-376 Sequence 376, App
41	1806	100.0	344	6	US-10-121-042-376 Sequence 376, App
42	1806	100.0	344	6	US-10-121-055-376 Sequence 376, App
43	1806	100.0	344	6	US-10-121-059-376 Sequence 376, App
44	1806	100.0	344	6	US-10-124-822-376 Sequence 376, App
45	1806	100.0	344	6	US-10-124-822-376 Sequence 376, App

ALIGNMENTS

RESULT 1
US-09-978-403A-523
; Sequence 523, Application US/09978403A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISVAIFGTGLAALCLFQGVPRVSGDATFPKAMDNTVRQGSATLRCTID 60
Db 1 MKTIQPKMHNISVAIFGTGLAALCLFQGVPRVSGDATFPKAMDNTVRQGSATLRCTID 60
QY 61 NRVTRVAMLNRSTILYAGNDKWCIDPRVLLSNTQTOYSIEIONVDVYDEGPYTCVQTD 120
Db 61 NRVTRVAMLNRSTILYAGNDKWCIDPRVLLSNTQTOYSIEIONVDVYDEGPYTCVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSISINEGNISLTCTIATGRPEPTVTRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSISINEGNISLTCTIATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREGSGDYECSSANDVAAPVVRKVTVNTPPYISEAKGCVPGQKGT 240
Db 181 SEDEYLEIQGITREGSGDYECSSANDVAAPVVRKVTVNTPPYISEAKGCVPGQKGT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKVENRPFLSKLIFFENVSEHDYGNVTCVASNK 300
Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKVENRPFLSKLIFFENVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPQAVSEVSNSTSRAGCWLPLPLVHLHLKE 344
Db 301 LGHTNASIMLFGPQAVSEVSNSTSRAGCWLPLPLVHLHLKE 344

RESULT 2

US-09-978-544A-523
; Sequence 523, Application US/09978544A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC13
; CURRENT APPLICATION NUMBER: US/09/978,544A
; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
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; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/079923
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; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203

; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
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; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
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; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHSISMAIFTGLAALCLFQGVPRSGDATEPKAMDNTVRQGSATLRCTID 60
Db 1 MKTIQPKMHSISMAIFTGLAALCLFQGVPRSGDATEPKAMDNTVRQGSATLRCTID 60
QY 61 NRVTRYAWLNRSTIYAGNDKWCIDPRVLLSNTQTOYSIEIONVDVYDEGPTYCSVQTD 120
Db 61 NRVTRYAWLNRSTIYAGNDKWCIDPRVLLSNTQTOYSIEIONVDVYDEGPTYCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICATGRPEPTVTWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTICATGRPEPTVTWRHISPKAVGFV 180
QY 181 SEDEYIEIQGITREOSGDYECASANDVAAPVVRVKVTVNPYIIEAKGTGVPVGOKGT 240
Db 181 SEDEYIEIQGITREOSGDYECASANDVAAPVVRVKVTVNPYIIEAKGTGVPVGOKGT 240
QY 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKVENRPFSLKIFPNVSEHDYGNVTCVASK 300
Db 241 LQCEASAVPSAEFQWKDKRLIEGKKGVKVENRPFSLKIFPNVSEHDYGNVTCVASK 300
QY 301 IGHFNASIMLFPGAVSEVSNSTSRACGCVWLLPLVLHLLEKF 344
Db 301 IGHFNASIMLFPGAVSEVSNSTSRACGCVWLLPLVLHLLEKF 344

RESULT 3
US-09-978-681A-523
; Sequence 523, Application US/09978681A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC18
CURRENT APPLICATION NUMBER: US/09/978,681A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079656
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PRIOR APPLICATION NUMBER: 60/079728
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PRIOR APPLICATION NUMBER: 60/079786
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PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
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PRIOR APPLICATION NUMBER: 60/080107
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
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PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
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PRIOR APPLICATION NUMBER: 60/082568
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PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639

; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMNSISWAIETGIALCLFQGVVRSQDATEPKAMDNVTVRQGESATLCTID 60
Db 1 MKTIQPKMNSISWAIETGIALCLFQGVVRSQDATEPKAMDNVTVRQGESATLCTID 60
QY 61 NRYTRVAVLNKSTILYAGNDKWCLDPVYLLSNTQYQYSEIQNVVYDEGPTYSVQTD 120
Db 61 NRYTRVAVLNKSTILYAGNDKWCLDPVYLLSNTQYQYSEIQNVVYDEGPTYSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINMGNNISLTCIATGRPEPTYWRHISPRAGVFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINMGNNISLTCIATGRPEPTYWRHISPRAGVFV 180
QY 181 SEDEYLEIQGTRQSGDYECASASNDVAAPVVRKRVTVNYPPIYSEAKGTGVPYQOKGT 240
Db 181 SEDEYLEIQGTRQSGDYECASASNDVAAPVVRKRVTVNYPPIYSEAKGTGVPYQOKGT 240
QY 241 LOCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
Db 241 LOCEASAVPSAEFQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLEFGPAVSEVNGTSRRAGCWWLLPLVLHLLKF 344
Db 301 LGHTNASIMLEFGPAVSEVNGTSRRAGCWWLLPLVLHLLKF 344

RESULT 4
US-09-978-757A-523
; Sequence 523, Application US/09978757A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978,757A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPRAGVF 180
DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPRAGVF 180
QY 181 SEDEYLEIQTREQSGDYECSSASNDYAAPVRRVRYTVNYPPIYSEAKGTGPVQOKGT 240
DB 181 SEDEYLEIQTREQSGDYECSSASNDYAAPVRRVRYTVNYPPIYSEAKGTGPVQOKGT 240
QY 241 LQCEASAVPSAEFQWYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
DB 241 LQCEASAVPSAEFQWYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPAVSEVNGTSRRAGCWLPLLVHLLKE 344
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RESULT 5
US-09-978-564A-523

; Sequence 523, Application US/09978564A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; PRIOR APPLICATION NUMBER: 2001-10-16
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Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T I O P K M H N S I S W A I F T G L A L C L F O G V P V R S G D A T F P K A M D N V T V R O G E S A T L R C T I D 60
Db 1 M K T I O P K M H N S I S W A I F T G L A L C L F O G V P V R S G D A T F P K A M D N V T V R O G E S A T L R C T I D 60
QY 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T Q T O Y S I E I O N V D V Y D E G P Y T C S V Q T D 120
Db 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T Q T O Y S I E I O N V D V Y D E G P Y T C S V Q T D 120
QY 121 N H P K T S R V H L I V O V S P K I V E I S S D I S I N E G N N I S L T C I A T G R P E P T V T W R H I S P K A V G F V 180
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|||||
Db 121 NHPKTSRVHLIVOVSPKIVEISSDISINENNNISLTCIATGREPTVTWRHISPKAVGFV 180
QY 181 SEDEYLEIQITREQSGDYECSSASNDVAAPVBRVKYTVNYPYISSEAKGTGVPVQOKGT 240
Db 181 SEDEYLEIQITREQSGDYECSSASNDVAAPVBRVKYTVNYPYISSEAKGTGVPVQOKGT 240
QY 241 LOCEASAVPSAEFQWYKDKRLIEGKKGVENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEFQWYKDKRLIEGKKGVENRPFLSKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLVHLHLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLVHLHLKF 344

RESULT 6
US-09-999-831A-523
; Sequence 523, Application US/09999831A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PlC68
; CURRENT APPLICATION NUMBER: US/09/999,831A
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 523
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-999-831A-523
```

```
Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T I O P K M H N S I S W A I F T G L A L C L F O G V P V R S G D A T F P K A M D N V T V R O G E S A T L R C T I D 60
Db 1 M K T I O P K M H N S I S W A I F T G L A L C L F O G V P V R S G D A T F P K A M D N V T V R O G E S A T L R C T I D 60
QY 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T Q T O Y S I E I O N V D V Y D E G P Y T C S V Q T D 120
Db 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T Q T O Y S I E I O N V D V Y D E G P Y T C S V Q T D 120
```


[illegible]

RESULT 7
US-09-999-829A-523
; Sequence 523, Application US/09999829A

```

: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C61
: CURRENT APPLICATION NUMBER: US/09/999,829A
: CURRENT FILING DATE: 2002-03-19
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 523
: LENGTH: 344
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-999-829A-523

```

	Query Match	100.0%;	Score 1806;	DB 5;	Length 344;
	Best Local Similarity	100.0%;	Pred. No. 2.2e-113;		
	Matches 344;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 MKTIQPKMHNISMAIFTGLAALCLFQGVPVRSRGDAFFKAMDNTVTROGESATLRCTTD	60			
Dd	1 MKTIQPKMHNISMAIFTGLAALCLFQGVPVRSRGDAFFKAMDNTVTROGESATLRCTTD	60			
QY	61 NRYTRVAWLNRSTILYAGNDKWCILDPRVLLSNTQTQYSIEIQNVDDYDEGPTCSGYTD	120			
Dd	61 NRYTRVAWLNRSTILYAGNDKWCILDPRVLLSNTQTQYSIEIQNVDDYDEGPTCSGYTD	120			

QY	121	NHKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGREPTVTWRHISPKAVGFV	180
Dd	121	NHPRTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGREPTVTWRHISPKAVGFV	180
QY	181	SEDEYLEIOGITREQSGDYECASANDVAAPVVRRYKVTVNYPYISEAKGTGPVGQKG	240
Dd	181	SEDEYLEIOGITREQSGDYECASANDVAAPVVRRYKVTVNYPYISEAKGTGPVGQKG	240
QY	241	LQCEASAVPSAEFQWYKDKRLIEGKKGVKENRPFSLKLIENVSEHDYGNVTCVASNK	300
Dd	241	LQCEASAVPSAEFQWYKDKRLIEGKKGVKENRPFSLKLIENVSEHDYGNVTCVASNK	300
QY	301	LGHTNASIMLFGPGAVSEVNGTSRRAGCVMLPLVLHLILKF	344
Dd	301	LGHTNASIMLFGPGAVSEVNGTSRRAGCVMLPLVLHLILKF	344

RESULT 8
US-09-978-375A-523
; Sequence 523, Application US/09978375A

```

: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C24
: CURRENT APPLICATION NUMBER: US/09/978,375A
: CURRENT FILING DATE: 2002-04-19
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 523
: LENGTH: 344
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-978-375A-523

```

```
Query Match          100.0%; Score 1806; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.2e-113;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 61 NRVTNVAWLNRSITLYAGNDKWCIDPRVLLSNTQTQYSIEIONVDVYDEGPYTCVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISITCIATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISITCIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITRQSGDYECASANDVAAPVYRVKVTVNPYPISEAKGTGVPVGQGT 240
Db 181 SEDEYLEIQGITRQSGDYECASANDVAAPVYRVKVTVNPYPISEAKGTGVPVGQGT 240
QY 241 LOCEASAVPSAEQWYKDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEQWYKDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGGAVSEVSNSTSRAGCWWLLPLVLHLLEKF 344
Db 301 LGHTNASIMLFGGAVSEVSNSTSRAGCWWLLPLVLHLLEKF 344

RESULT 9
US-09-978-423A-523
; Sequence 523, Application US/09978423A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704

;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082700
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
Query Match 100.0%; Score 1806; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIQPKMHNISMAFTGLALCLFQGVPRVRSQDATFPKAMNVTVRQGESATLRCITID 60
DB 1 MKTIQPKMHNISMAFTGLALCLFQGVPRVRSQDATFPKAMNVTVRQGESATLRCITID 60
QY 61 NRVTRVAMLNRSITLYAGNDKWCLEPRVLLSNTQYISIEIQNVDDYDEGPTCSVQTD 120
DB 61 NRVTRVAMLNRSITLYAGNDKWCLEPRVLLSNTQYISIEIQNVDDYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
DB 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQITREQSGDYECASANDVAAPVRRYKVTVNPYISEAKGTGVVGQKGT 240
DB 181 SEDEYLEIQITREQSGDYECASANDVAAPVRRYKVTVNPYISEAKGTGVVGQKGT 240
QY 241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKENRPFSLKLIFFNVSEHDYGNATCVASNK 300
DB 241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKENRPFSLKLIFFNVSEHDYGNATCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNSTSRAGCWWLLPLLVLHLLKF 344
DB 301 LGHTNASIMLFGPGAVSEVSNSTSRAGCWWLLPLLVLHLLKF 344
RESULT 10
US-10-013-921A-523
; Sequence 523, Application US/10013921A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
; FILE REFERENCE: P2630P1C84
; CURRENT APPLICATION NUMBER: US/10/013,921A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

[illegible]


```

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

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```

Query Match      100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MKTIQPKMHNSTSWAIFGTGLAALCLFQGVPRSGDAFPKAMDNVYRQGESATLRCCTID 60
Db 1 MKTIQPKMHNSTSWAIFGTGLAALCLFQGVPRSGDAFPKAMDNVYRQGESATLRCCTID 60
QY 61 NRYTRVAMLNSTILYAGNDKWCLDPVYVLLNSTQTOYSIEIQNVVDYDEGPYTCVQTD 120
Db 61 NRYTRVAMLNSTILYAGNDKWCLDPVYVLLNSTQTOYSIEIQNVVDYDEGPYTCVQTD 120
QY 121 NHEKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFV 180
Db 121 NHEKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECSSASNDVAPVRRKVTVNYPPYISAKGTGPVQCKGT 240
Db 181 SEDEYLEIQGITREQSGDYECSSASNDVAPVRRKVTVNYPPYISAKGTGPVQCKGT 240
QY 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKNRPFLSKLIFFNWSEHDYGNVTCVASNK 300
Db 241 LOCEASAVPSAEFQWKDKRLIEGKKGVKNRPFLSKLIFFNWSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGPQAVSEVNGTSRRAGCVLLPLVLHLLKF 344
Db 301 LGHTNASIMLFGPQAVSEVNGTSRRAGCVLLPLVLHLLKF 344

```

```

RESULT 11
US-10-013-929A-523
; Sequence 523, Application US/10013929A
; GENERAL INFORMATION:

```

```

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

```

```

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC89
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKTIQPKMHNSTISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVOGESATLRCTID 60
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QY 121 NHPKTSRVHLIYQVSPKIVEISSDISINEGNISITCTATGRPEPTVWRHISPKAVGFV 180
DB 121 NHPKTSRVHLIYQVSPKIVEISSDISINEGNISITCTATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQTREQSGDYECASASNDVAVYRVKVTYVNPPIYSEAKGTGVPVGQKGT 240
DB 181 SEDEYLEIQTREQSGDYECASASNDVAVYRVKVTYVNPPIYSEAKGTGVPVGQKGT 240
QY 241 LOCEASAVPSAFQWYKDKRLIEGKKGVYENRPFLLSKLIFPNVSEHDYGNITCVASNK 300
DB 241 LOCEASAVPSAFQWYKDKRLIEGKKGVYENRPFLLSKLIFPNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVHLLKF 344
DB 301 LGHTNASIMLFGPGAVSEVSNGTSSRRAGCVWLLPLLVHLLKF 344

RESULT 12
US-10-013-918A-523
; Sequence 523, Application US/10013918A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC77
CURRENT APPLICATION NUMBER: US/10/013,918A
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNSTISWAIFTGLALCLFQGVPRSGDATFRKAMDNVTVRGESAATLRCTID 60
Db 1 MKTIQPKMHNSTISWAIFTGLALCLFQGVPRSGDATFRKAMDNVTVRGESAATLRCTID 60
QY 61 NRYTRVAMLNRSITLLYAGNDKCLDPRVVLISNTQOTYSIEIQNVVDYDEGPTCSVQTD 120
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Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQITREQSGDYECASNDVAAPYVRKVTVNPPYISEAKGTGVPVGOKGT 240
Db 181 SEDEYLEIQITREQSGDYECASNDVAAPYVRKVTVNPPYISEAKGTGVPVGOKGT 240
QY 241 IQCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSK 300
Db 241 IQCEASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSK 300
QY 301 IGHNTASIMLFGGAVSEVSNSTSRACGCVLLPLVLHLILKE 344
Db 301 IGHNTASIMLFGGAVSEVSNSTSRACGCVLLPLVLHLILKE 344

RESULT 13
US-10-017-082A-523

; Sequence 523, Application US/10017082A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Geritsen, Mary E.
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; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C71
; CURRENT APPLICATION NUMBER: US/10/017,082A
; PRIOR FILING DATE: 2002-03-25
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29

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; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

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Query Match          100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 M K T I O P R M H N S I S W A I F T G L A L C I F Q G V P V R S G D A T F P K A M D N V T V R Q G E S A T L R C T I D 60
Db 1 M K T I O P R M H N S I S W A I F T G L A L C I F Q G V P V R S G D A T F P K A M D N V T V R Q G E S A T L R C T I D 60
QY 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T O T O Y S I E I Q N V D V Y D E G P Y T C S V Q T D 120
Db 61 N R V T R V A W L N R S T I L Y A G N D K W C L D P R V L L S N T O T O Y S I E I Q N V D V Y D E G P Y T C S V Q T D 120
QY 121 N H P K T S R V H L I V O V S K R I V E I S S D I S I N E G N N I S I L T C I A T G R P E F T V T W R H I S P K A V G F V 180
Db 121 N H P K T S R V H L I V O V S K R I V E I S S D I S I N E G N N I S I L T C I A T G R P E F T V T W R H I S P K A V G F V 180
QY 181 S E D E Y L E I O G I T R E S G D Y E C S A S N D V A P V R V R K V T V N Y P P Y I S E A K G T G V P V G O K T 240

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Db 181 SEDEYLEIQGITREQSGDYECASASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGT 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344

RESULT 14

US-10-119-480-126

; Sequence 126, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 126
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-126

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLAALCLFGGVPRSGDATEPKAMDNTVRGESAATLRCTID 60
Db 1 MKTIQPKMHNISWAIFTGLAALCLFGGVPRSGDATEPKAMDNTVRGESAATLRCTID 60
QY 61 NRYTRVAMLNRSITLLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTD 120
Db 61 NRYTRVAMLNRSITLLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECASASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQGITREQSGDYECASASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGT 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344

RESULT 15

US-10-121-049-376

; Sequence 376, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-376

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-113;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMHNISWAIFTGLAALCLFGGVPRSGDATEPKAMDNTVRGESAATLRCTID 60
Db 1 MKTIQPKMHNISWAIFTGLAALCLFGGVPRSGDATEPKAMDNTVRGESAATLRCTID 60
QY 61 NRYTRVAMLNRSITLLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTD 120
Db 61 NRYTRVAMLNRSITLLYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVWRHISPKAVGFV 180
QY 181 SEDEYLEIQGITREQSGDYECASASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQGITREQSGDYECASASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGT 240
QY 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
Db 241 LQCEASAVPSAEFQWKDDKRLIEGKKGVKVENRPFSLKIFENVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSTRAGCWWLLPLVLHLLKF 344

Search completed: July 12, 2002, 00:42:36
Job time: 574 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2002, 23:01:37 ; Search time 67.53 Seconds

(without alignments)
489.482 Million cell updates/sec

Title: US-09-700-397-3

Perfect score: 1806

Sequence: 1 MKTIQPKMHSISWAFITGL.....RRAGCVWLLPLVHLHLKF 344

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_71:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639.5	90.8	344	2	neurotrophin - rat
2	1285.5	71.2	338	2	opioid-binding pro
3	1268	70.2	345	2	opioid-binding pro
4	1266	70.1	345	2	opioid-binding pro
5	1259	69.7	345	2	opioid-binding pro
6	936.5	51.9	338	2	50K glycoprotein p
7	931.5	51.6	338	2	limbic-system-asso
8	297.5	16.5	333	2	amalgam protein pr
9	283.5	15.7	725	1	neural cell adhesi
10	283.5	15.7	725	1	neural cell adhesi
11	279.5	15.5	1115	1	neural cell adhesi
12	279.5	15.5	1091	1	neural cell adhesi
13	278.5	15.4	4162	2	neural cell adhesi
14	277.5	15.4	858	1	neural cell adhesi
15	277.5	15.4	1088	1	neural cell adhesi
16	276	15.3	761	1	neural cell adhesi
17	275.5	15.3	853	1	neural cell adhesi
18	273.5	15.1	725	2	neural cell adhesi
19	272.5	15.1	1323	2	neural cell adhesi
20	270.5	15.0	1092	1	neural cell adhesi
21	261.5	14.5	1091	2	neural cell adhesi
22	259	14.3	7962	2	neural cell adhesi
23	254.5	14.1	5175	2	neural cell adhesi
24	254.5	14.1	5198	2	neural cell adhesi
25	249.5	13.8	1040	2	neural cell adhesi
26	246.5	13.6	1018	2	neural cell adhesi
27	243.5	13.5	1021	2	neural cell adhesi
28	243.5	13.5	1036	2	neural cell adhesi
29	241.5	13.4	1018	2	neural cell adhesi

30	241.5	13.4	1020	2	neural cell surf
31	240	13.3	3707	2	heparan sulfate pr
32	235	13.0	662	2	hypothetical prote
33	234.5	13.0	1040	2	axonal glycoprotei
34	232.5	12.9	2783	2	hypothetical prote
35	230.5	12.8	868	2	CD22 homolog/B lym
36	227.5	12.6	1051	2	kinase-like protei
37	226	12.5	6642	2	protein UNC-89 - C
38	225	12.5	4391	2	perlecan precursor
39	221.5	12.3	862	2	differentiation an
40	221	12.2	1896	2	Down syndrome cell
41	220.5	12.2	898	2	fasciclin II precu
42	219	12.1	1091	2	glial cell membran
43	218.5	12.1	1612	2	dufil protein - mo
44	215.5	11.9	1239	1	neuroglial - fruit
45	214.5	11.9	1070	2	protein-tyrosine k

ALIGNMENTS

RESULT 1
neurotrophin - rat
156551
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrophin defines a new subfamily of differentially expresse
A;Reference number: I56551; MUID:95198094
A;Accession: I56551
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-

Query Match 90.8%; Score 1639.5; DB 2; Length 344;
Best Local Similarity 92.9%; Pred. No. 1.7e-113;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY	12	ISWAFITGLALCLF---QGVPRSGDATFPKAMDNTVRQGESATLRCITIDNRVTRVAM	68
Db	9	LPWKCLVYVSLRLFLVPTGPVRSQDATFPKAMDNTVRQGESATLRCITIDNRVTRVAM	68
QY	69	INRSTIYAGNDKWCIDPRVLLSMTQOYSIEIQNVQVYDEGPTCSVQTDNHPKTSRV	128
Db	69	INRSTIYAGNDKWCIDPRVLLSMTQOYSIEIQNVQVYDEGPTCSVQTDNHPKTSRV	128
QY	129	HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVEDEYLEI	188
Db	129	HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVEDEYLEI	188
QY	189	QGITREQSGDYECASNDVAAPVVRKVTYVNPPIYISEAKGTGYPVGQKGTIQCEASAV	248
Db	189	QGITREQSGDYECASNDVAAPVVRKVTYVNPPIYISEAKGTGYPVGQKGTIQCEASAV	248
QY	249	PSAEFQWKDDKRLIEGKKGKGVKVENPFLSKLIFNVSEHDYGNITCVASNKLGHTNASI	308
Db	249	PSAEFQWKDDKRLIEGKKGKGVKVENPFLSKLIFNVSEHDYGNITCVASNKLGHTNASI	308
QY	309	MLFGPGAVSEVSNQTSRRAGCVWLLPLVHLHLKF	344
Db	309	MLFGPGAVSEVSNQTSRRAGCVWLLPLVHLHLKF	344

RESULT 2
JCI1238
opioid-binding protein (clone DU21) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000

C:Accession: JC1238
R:Lippman, D.A.; Lee, N.M.; Ioh, H.H.
Gene 117, 249-254, 1992
A:Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain
A:Reference number: JC1238; MUID:92347701
A:Accession: JC1238
A:Molecule type: mRNA
A:Residues: 1-338 <LIP>
A:Cross-references: GB:M88709; NID:g203245; PIDN:AAA40858.1; PID:g203246
A:Experimental source: brain
C:Genetics:
A:Gene: OBCAM
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 71.2%; Score 1285.5; DB 2; Length 338;
Best Local Similarity 71.6%; Pred. No. 2.1e-87;
Matches 242; Conservative 35; Mismatches 60; Indels 1; Gaps 1;

QY 8 MHSISMAIFTLALCLFQGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 67
DB 1 MHPAYWIVFSATLALFLIPGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 60
QY 68 WLNRSSTLYAGNDKWCCLDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSR 127
DB 61 WLNRSSTLYAGNDKWSIDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSR 120
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYL 186
DB 121 VHLIVQSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYL 180
QY 187 EIQTREQSGDYECASANDVAAPVRRVKVTNYPPISEAKGTGVPVQKGTLOCEAS 246
DB 181 EISDIKRDQSGEYECASALNDVAAPDVRRVKVTNYPPISEAKGTGVPVQKGTLOCEAS 240
QY 247 AVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 306
DB 241 AVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 300
QY 307 SIMLEFGPAGVSEVNGTSRRAGCWLPLPLVHLHLKF 344
DB 301 SITLYGPGAVIDGVNSASRALACLWLSGTFPAHFFIKF 338

RESULT 3
JC4025
opiod-binding cell adhesion protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Mar-2000
C:Accession: JC4025
R:Shark, K.B.; Lee, N.M.
Gene 155, 213-317, 1995
A:Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a huma
A:Reference number: JC4025; MUID:95237612
A:Accession: JC4025
A:Molecule type: mRNA
A:Residues: 1-345 <SHA>
A:Cross-references: GB:L34774; NID:g514373; PIDN:AAA36387.1; PID:g514374
A:Experimental source: brain
C:Comment: This protein binds opiod alkaloids in the presence of acidic lipids, exhibit
C:Genetics:
A:Gene: GDB:OPCML; OBCAM; OPCM
A:Cross-references: GDB:251677; OMIM:600632
A:Map position: 11pter-11qter
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 70.2%; Score 1268; DB 2; Length 345;
Best Local Similarity 71.2%; Pred. No. 4.2e-86;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

QY 12 ISMAFTGLALCLF--QGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 68
DB 12 ISMAFTGLALCLF--QGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 68

DB 9 LPWKCLVAVSLRLFLVPTGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 68
QY 69 LNRSTLYAGNDKWCCLDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSRV 128
DB 69 LNRSTLYAGNDKWSIDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSRV 128
QY 129 HLIQVSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYLE 187
DB 129 HLIQVSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYLE 188
QY 188 IQGTRQSGDYECASANDVAAPVRRVKVTNYPPISEAKGTGVPVQKGTLOCEASA 247
DB 189 ISDIKRDQSGEYECASALNDVAAPDVRRVKVTNYPPISEAKGTGVPVQKGTLOCEASA 248
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 307
DB 249 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 308
QY 308 IMLEFGPAGVSEVNGTSRRAGCWLPLPLVHLHLKF 344
DB 309 ITLYGPGAVIDGVNSASRALACLWLSGTFPAHFFIKF 345

RESULT 4
S03199
opiod-binding protein OPCAM precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 17-Mar-2000
C:Accession: S03199
R:Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S
EMBO J. 8, 489-495, 1989
A:Title: Molecular characterization of a new immunoglobulin superfamily protein wit
A:Reference number: S03199; MUID:89251576
A:Accession: S03199
A:Molecule type: mRNA
A:Residues: 1-345 <SCH>
A:Cross-references: EMBL:X12672; NID:g585; PIDN:CAA31192.1; PID:g586
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-1
C:Keywords: transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-345/Product: opiod-binding protein OPCAM #status predicted <MAT>

Query Match 70.1%; Score 1266; DB 2; Length 345;
Best Local Similarity 71.6%; Pred. No. 5.9e-86;
Matches 240; Conservative 34; Mismatches 57; Indels 4; Gaps 2;

QY 14 MAFTGLALCLF--QGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 70
DB 11 WKCLVAVSLRLFLVPTGVPRSGDATFPKAMDNTVRQGESATLRCTIDNRVTRVA 70
QY 71 RSTILYAGNDKWCCLDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSRVHL 130
DB 71 RSTILYAGNDKWSIDPRVLLSNQTQYSIEIQNVYDEGPYTCVQTDNHPKTSRVHL 130
QY 131 IVQVSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYLEIQ 189
DB 131 IVQVSPKIVEISSDISINEGNNISLTGATGRPEPTVTRHISPK-AVGFSSEDEYLEIQ 188
QY 190 GTRQSGDYECASANDVAAPVRRVKVTNYPPISEAKGTGVPVQKGTLOCEASAVP 249
DB 191 DIKRDQSGEYECASALNDVAAPDVRRVKVTNYPPISEAKGTGVPVQKGTLOCEASAVP 250
QY 250 SAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 309
DB 251 MAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNA 310
QY 310 LEFGPAGVSEVNGTSRRAGCWLPLPLVHLHLKF 344
DB 311 LYGPGAVIDGVNSASRALACLWLSGTFPAHFFIKF 345

RESULT 5

A:Residues: 1-348, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MOPS', 593, 'S', 595-599, 'P', 601, 'L'
A:Cross-references: EMBL:X00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R:Santoni, M.J.; Barthels, D.; Barbás, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
Nucleic Acids Res. 15, 8621-8641, 1987
A:Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
A:Reference number: S00844; MUID:88067687
A:Accession: S00844
A:Molecule type: mRNA
A:Residues: 529-809, 1077-1115 <SAN>
A:Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A:Reference number: S00382; MUID:88283628
A:Accession: S00384
A:Molecule type: DNA
A:Residues: 642-1115 <BAR>
A:Cross-references: EMBL:X07195
R:Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A:Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A:Reference number: A28281; MUID:88347737
A:Accession: A28281
A:Molecule type: mRNA
A:Residues: 804-1081 <BA3>
A:Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
R:Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A:Title: Structural and immunological characterization of the amino-terminal domain of m
A:Reference number: A44290; MUID:86140120
A:Accession: A44290
A:Molecule type: protein
A:Residues: 20-36 <ROU>
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C:Genetics:
A:Gene: NCAM
A:Map position: 9
A:Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1115/Product: neural cell adhesion molecule, long domain splice form #status expe
F:20-809, 1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
F:20-711/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-290/Domain: immunoglobulin homology <IMM3>
F:262-272/Region: NCAM binding #status predicted
F:323-388/Domain: immunoglobulin homology <IMM4>
F:420-482/Domain: immunoglobulin homology <IMM5>
F:519-596/Domain: fibronectin type III repeat homology <FN3A>
F:625-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <TM>
F:730-1115/Domain: intracellular #status predicted <INT>
F:41-96, 139-189, 235-288, 330-386, 427-480/Disulfide bonds: #status predicted
F:222, 316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.7%;	Score 283.5;	DB 1;	Length 1115;
Best Local Similarity	25.8%;	Pred. No. 7.3e-13;		
Matches	75;	Conservative 45;	Mismatches 130;	Indels 41;
				Gaps 7;
QY	44	NTVVRQGESATLRCTIDNRVTRVAMLNRSSTILVAGNDKWCIDPRVY-----LLSNTQ	95	
Db	222	NATANLGGSVTLVCDADG-----FPEPTM-----SWTKDGEPIENEEDEDRSRSSVS	268	
QY	96	TQYSIEIQAVDYDEGPYTCVSQTDHHPKTSRHALIVQSPKIVEISSDISINEGNNISL	155	
		: : : : : : :		: : :
Db	269	DSSEVTIRAVDKNDEAEIVCIAENAGGEQDASIHKLKFAKPKITYVENQTMELLEQVTL	328	

[illegible]

RESULT 11

neural cell adhesion molecule 1 - African clawed frog
N/Alternate names: N-CAM 1
C/Species: *Xenopus laevis* (African clawed frog)
C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: J50099
R/Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A/Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as
A/Reference number: J50099; MUID:98204770
A/Accession: J50099
A/Molecule type: mRNA
A/Residues: 1-725 <KUD>
A/Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A/Experimental source: heart
C/Comment: This protein mediates and regulates various cell-cell interactions thrc
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology
F:413-475/Domain: immunoglobulin homology <IMM>
F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match	15.5%;	Score 279.5;	DB 2;	Length 725;
Best Local Similarity	27.9%;	Pred. No. 8.3e-13;		
Matches	80;	Conservative	50;	Mismatches 120;
				Indels 37;
				Gaps 11;

```

QY 44 NVTVRGESHATLRCTIDN-RVTRVAMINRSTILYAGDNKWKCLDPVVLLSNTOQOYSLEI 102
    | | : | | | | : | | : | | : | | : | | : | |
Db 219 NATAKMAESVLSCLDADGFPDPPEISWLKKEPIEDGEEK-----ISFNEDQSEMTI 269
QY 103 QNVDVYDEGPRYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
    : | | | | : | | : | | | | : | | : | | | | : | |
Db 270 HHVEKDEAEYSCLANNQAGEAEATILKLKYAKPKIYVENKTA-V-ELDEITLTCESASGD 328
QY 163 PEPTVTW----RHISPKAV--GFVSEDEYLEIQGITRE----QSGBYECSASNDVAAP 210
    | | : | | | | : | | : | | : | | : | | | | : | |
Db 329 PIPSITWRRAVRNISRISSEATLLDGHIVYKHEHIRMSALTILKDIQYTDAGEYECIASNPIGVD 388
QY 211 VVRRAKVTYNNRPYISEAKGTGVPV-----GQKGTLOCEASAVPSAEFQWYKDKDLIE 264
    : : : | | | | : | | : | | : | | | | : | | : | |
Db 389 -MQAMTFEYQAPKI---RG---PVVYITWEGNPVNITCEVFAHPRRAVATWFRDQGLPS 441
QY 265 GK-KGVAKVENRPFLSKLIFENVSEHDYGNITCVASNKLGHTNASIML 310
    : : : | | | | | | | : | | | | | | | : | | : | |
Db 442 SNFSNIIKITSGPTSSSLEVPDSENDFGNYNCTAINTIGHEFSEFIL 488

```

RESULT 12

neural cell adhesion molecule long domain form precursor - chicken
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A43613; B43613; A25435; B25435; A46550; S36950; A44369; A60852; S2966
R;Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Brackenbury, R.;
Science 236, 799-806, 1987
A;Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, ce
A;Reference number: A43613; MUID:87206190
A;Accession: A43613

A:Molecule type: mRNA
A:Residues: 1-175 <CU2>
A:Cross-references: GB:M15860
A:Accession: B43613
A:Molecule type: protein
A:Residues: 20-44,120-127,202-221,320-342,399-415,640-659,822-828 <CUN>
A:Note: Asn-222 probably binds carboxylate; Asn-226 probably does not
R:Hempferly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
A:Title: Sequence of a cDNA clone encoding the polysialic acid-rich and cytoplasmic domain of the neural cell adhesion molecule
A:Reference number: A25435; MUID:86206089
A:Accession: A25435
A:Molecule type: mRNA
A:Residues: 128-1091 <HEM>
A:Cross-references: GB:M13210
A:Accession: B25435
A:Molecule type: protein
A:Residues: 128-140,222-240,428-439,611-631,744-760,763-781,1080-1084 <HE2>
R:Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.
J. Cell Biol. 103, 1431-1439, 1986
A:Title: Cell surface modulation of the neural cell adhesion molecule resulting from alternative splicing
A:Reference number: A46550; MUID:87033934
A:Accession: A46550
A:Molecule type: DNA
A:Residues: 810-1070 <MUR>
A:Cross-references: GB:X04479
R:Sasner, M.; Covault, J.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S36950
A:Accession: S36950
A:Molecule type: DNA
A:Residues: 1-17 <SAS>
A:Cross-references: EMBL:X70342; NID:g417631; PIDN:CAA49807.1; PID:g417632
R:Colwell, G.; Li, B.; Forrest, D.; Brackenbury, R.
Genomics 14, 875-882, 1992
A:Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A:Reference number: A44369; MUID:93122797
A:Accession: A44369
A:Molecule type: DNA
A:Residues: 1-17 <COE>
A:Cross-references: EMBL:Z12128; NID:g63653; PIDN:CAA78113.1; PID:g63654
A:Experimental source: White Leghorn
R:Coyle, G.J.; Loewy, A.; Cross, N.V.; Akesson, R.; Glaser, L.
J. Cell Biol. 103, 1739-1744, 1986
A:Title: Topographic localization of the heparin-binding domain of the neural cell adhesion molecule
A:Reference number: A60852; MUID:87057627
A:Accession: A60852
A:Molecule type: protein
A:Residues: 20-29 <COL>
R:Rao, Y.; Wu, X.F.; Garipey, J.; Rutishauser, U.; Sin, C.H.
J. Cell Biol. 118, 937-949, 1992
A:Title: Identification of a peptide sequence involved in homophilic binding in the neural cell adhesion molecule
A:Reference number: A43280; MUID:92363934
A:Contents: annotation; homophilic binding region
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule
C:Comment: Various forms of NCAM are produced by alternative splicing.
C:Keywords: neural cell adhesion molecule; fibronectin type III repeat homology; signal sequence; alternative splicing; brain; cell adhesion; duplication; heparin binding; duplication; heparin binding; signal sequence
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1091/Product: neural cell adhesion molecule, long domain form #status experimental
F:20-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status experimental
F:20-711/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-289/Domain: immunoglobulin homology <IMM3>
F:262-271/Region: NCAM binding #status experimental
F:322-387/Domain: immunoglobulin homology <IMM4>
F:419-481/Domain: immunoglobulin homology <IMM5>
F:518-595/Domain: fibronectin type III repeat homology <FN3A>
F:624-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <TM>

F;730-1091/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-287,329-385,426-479/Disulfide bonds: #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;315,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.5%;	Score 279.5;	DB 1;	Length 1091;
Best Local Similarity	26.0%;	Pred. No. 1.4e-12;		
Matches	78;	Conservative	52;	Mismatches 131;
				Indels 39;
				Gaps 9;

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QY   31 VRSGDATEPKAMDNVTIROGESATLKTIDNRVTRVAWMLNRSITLLIAGNDKRCICDP RVVL    90
      || : : |       | | : : | | | |       | :         | :         : 
Db   214 VAROSTM-----NATANISQSVTLIACDADG-----FPEPTM-----TWTKDGEP IE    255

QY   91 LSNTOUOYSIE-----IQNVDDVEDEGYTCVSQTJDNHPKTSRVHLIVOVSPKIVEISS    143
      : : : | |     | : | | | | | |       : : : | | | | | : : 
Db   256 QEDNEEKYSFNVDGSELLIKVKDKSDEAEYCIAENKAGEODATHLKVFAPKPITYVEN    315

QY   144 DISINEGNNISLTICIATGREPTVTW----RHISPAKV--GFVSEDEYLIEOGITREQ-    195
      : : : | : | | | : | | : | | : | : | : | : : | : : | : : : 
Db   316 KTAHELEDOTILTCEASGDPIPSITWKSTRNISNEKTLDGRIIVRSHARVASILTKEI    375

QY   196 ----SGDYECESANDVAAPVVRKVTVNYPPYISEAKGTGVPOGKGTLQCEASAVP SA    251
      : : | | : | | | : : : : | | | :        : : : | | | | | | 
Db   376 QYTDAGEYVCITASNTIGÖD-SQÄMYLEVOYAPKLQGPVAVYTMESNQVNITCEYFAYP SA    434

QY   252 EFOWTKDKRLTECK-KGVAVENRPFLSKLIFENVSEHDYGNYTCVASNKLGHMTNASIML    310
      : : : | : | : | : : | | | | | | : | | | : | | | : : : | 
Db   435 VISNERFDGOLPSSNSNIKITYNTPSASTYLEVTPDSENDFGNYNCATAVNRIGCESSEFIL    494
```

RESULT 13

T42633

connectin/titin - chicken (fragment)
C:Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42633

C;Accession: T42633

R;Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, T. Biochem. Biophys. Res. Commun. 223, 160-164, 1996

Biochem. Biophys. Res. Commun. 223, 160-164, 1996

A;Title: A 11:5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/fin
A;Reference number: Z22221; MUID:96254045

A;Reference number: Z222221; MUID:96254043

A;Accession: T42633
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Status: preliminary; t

A;Molecule type: mRNA
A;Residues: 1-4162 <YAJ>

A;Residues: 1-4162 <YAJ>

A;Cross-references: EMBL:D833390; NILE
A;Experimental source: breast muscle

A; Experimental source: bread

C;keywords: skeletal muscle

Query Match	15.4%;	Score 278.5;	DB 2;	Length 4162;
-------------	--------	--------------	-------	--------------

```

Query Match      15.4%; Score 2/8.5; DB

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Best Local Similarity 27.3%; Pred. No. 9,2e-12;
Matches 78; Conservative 38; Mismatches 145; Indels 25; Gaps 7;

Matches 78; Conservative 38; Mismatches 145; Indels 25; Gaps 1,

QY 37 TEPKAMDNVTVRQESATLRCTI-DNRVTRVAMINRSTILYAGNDKWCCLDPVYLLSNTQ 95

37 TEPKAMDNVTVRQGESATLRCTI-DNRVIRVAVLNRSIILYAGNDKWCLEPRVVLSSNIQ 95

```

      :| : | :| : : | :| :
Db 3747 SFVKKPEFNVLSGENTFTTSIVKSCPLEVKKWFRGSIELAPGKH-----CNIT 3795

```

DD 3/47 SFVKKPEFNVLSGENTTFISIVKGSPLLEVKNWEGSLELAPGK-----CNI 3/92

QY 96 TQYSI---EIQNDVYDEGPYTCVQTDNHPKTSRYHLIVQVSPKIVEISSDISINEGNN 152

96 110YSL---EIONVDVDEGPTICSVOQIDNHPKISRHLVQVSFKLVEISSDISINEGNN 132

```

Db 3796 LQDSVAELLEFDVQPLQSGDYTCQVSNAGKISCPTHLEFVKEPAFVMKVNDSVEKGN 3855
      | | : : | | | | : : | | : : : : | |

```

DB 3796 LQDSVAELETEDVQPLQSGDYTCQVSNACKISCTIHLVKKEPAKVMKYNLDSVEKGN 3853

QY 153 ISLFCIATGRPEPTVM-----RHISPKAVGEVEDEYLEIQGTTREQSGDYECOSASN 205

153 ISLICIAGREPVIW-----KHLSPKAVGEVSEDEYLEIQGLIKRUSGDIELCSASN ZV3

Db 3856 L I E C T Y N G P R I S V F W K N G V I L K H S E K S I T T T E D S A I L E I P N S K L E D Q O Y S C H I E N 391

DD 3856 LITECTYIGTIPRISVIMKNGVILAKHSERCSIITIEISALBELPNSKLEDDGQISCHLEN 391

QY 206 DVAPVYRRYKVTVNPPY - ISEAKGTGYPVGQKGLQCEASAVPSAEFFQWYKDDKRLIE 264

206 DVAAPVKKVKVIVNIPPY - TSEAKGIGVPVGQKGI LQCEASAVPSAEF QMINDDAKLLE 204

Db 3916 DSGQDNCHGA-ITILEPPYFVTPLEPYQVTVGDSASIQQVAGTPEMITVSWYKGTKL-R 3973

DD 3916 DSGJDNCHGA-111LEPPYEV1VLEPVQV1VGDASLJCQVAGIPEMLVSM1AGDLKL-R 09/23

QY 265 GKKGVKVENRPFSLKLFENVSEHDYGNVTCVASNKLGHNASIML 310

QY 203 GNGVA VENEKPELSKLL EFNVS EHDIGNITL VASNKLGHI NASIML 310

Db 3974 G T A T V K M H F K N Q V A T L V F S Q Y D S D S D S G E Y I C K V E N T V G E A T S S L L 4019

DO 374 GIMVNHANQVAILVESQVDSDDSGEILCVENI VGEHISBBL 4013

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 12, 2002, 00:35:02 ; Search time 35.02 Seconds

(without alignments)
380.341 Million cell updates/sec

Title: US-09-700-397-3

Perfect score: 1806

Sequence: 1 MKTIQPKMHNISWAIPTGL.....RRAGCVLLPLVLHLLEKF 344

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1639.5	90.8	344	1	NTRI_RAT Q62718 rattus norv
2	1477.5	81.8	353	1	CEPU_CHICK Q90773 gallus gall
3	1305	72.3	337	1	G55A_CHICK Q98892 gallus gall
4	1268	70.2	345	1	OPCM_HUMAN Q14982 homo sapien
5	1266	70.1	345	1	OPCM_BOVIN P11834 bos taurus
6	1259	69.7	345	1	OPCM_RAT P32736 rattus norv
7	938.5	52.0	338	1	LAMP_CHICK Q98919 gallus gall
8	931.5	51.6	338	1	LAMP_HUMAN Q13449 homo sapien
9	926.5	51.3	338	1	LAMP_RAT Q62813 rattus norv
10	815	45.1	348	1	KILO_RAT Q92018 rattus norv
11	297.5	16.5	333	1	AMAL_DROME P15364 drosophila
12	283.5	15.7	725	1	NCA2_MOUSE P13594 mus musculu
13	283.5	15.7	1115	1	NCA1_MOUSE P13595 mus musculu
14	279.5	15.5	1091	1	NCA1_CHICK P13596 gallus gall
15	277.5	15.4	858	1	NCA1_RAT P16170 xenopus lae
16	277.5	15.4	1088	1	NCA1_XENLA P13592 homo sapien
17	276	15.3	761	1	NCA2_HUMAN P13591 homo sapien
18	276	15.3	848	1	NCA1_HUMAN P13836 bos taurus
19	275.5	15.3	853	1	NCA1_BOVIN P36335 xenopus lae
20	270.5	15.0	1092	1	NCA2_XENLA P14781 gallus gall
21	261.5	14.5	1010	1	CONT_CHICK Q24372 drosophila
22	255	14.1	359	1	LACH_DROME Q35136 mus musculu
23	251.5	13.9	837	1	NCA2_MOUSE Q26474 schistocerc
24	250	13.8	349	1	LACH_SCHAM Q02246 homo sapien
25	249.5	13.8	1040	1	AXO1_HUMAN Q12860 homo sapien
26	246.5	13.6	1018	1	CONT_HUMAN Q63198 rattus norv
27	243.5	13.5	1021	1	CONT_RAT P28685 gallus gall
28	243.5	13.5	1036	1	AXO1_CHICK P15394 homo sapien
29	241.5	13.4	837	1	NCA2_HUMAN P12960 mus musculu
30	241.5	13.4	1020	1	CONT_MOUSE Q05793 mus musculu
31	240	13.3	3707	1	PGBM_MOUSE P22063 rattus norv
32	234.5	13.0	1040	1	AXO1_RAT P98160 homo sapien
33	230	12.7	4393	1	PGBM_HUMAN

34	227.5	12.6	1051	1	PTK7_CHICK Q91048 gallus gall
35	221.5	12.3	862	1	CD22_MOUSE P35329 mus musculu
36	221	12.2	2012	1	DSCA_HUMAN O60469 homo sapien
37	220.5	12.2	898	1	FAS2_SCHAM P22648 schistocerc
38	215.5	11.9	1302	1	NRG_DROME P20241 drosophila
39	211.5	11.7	811	1	FS22_DROME P34083 drosophila
40	211.5	11.7	873	1	FS21_DROME P34082 drosophila
41	211.5	11.7	1070	1	PTK7_HUMAN Q13308 homo sapien
42	211.5	11.7	1461	1	NEO1_HUMAN Q92859 homo sapien
43	210	11.6	1914	1	KML5_HUMAN Q15746 homo sapien
44	204.5	11.3	1377	1	NEO1_RAT P97603 rattus norv
45	204	11.3	1443	1	NEO1_CHICK Q90610 gallus gall

ALIGNMENTS

RESULT	1	STANDARD	PRT	344 AA.
ID	NTRI_RAT			
AC	Q62718;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Neurotrophin precursor (GP65).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RX	MEDLINE=95198094; Pubmed=7891157;			
RA	Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,			
RA	Salzer J.L.;			
RT	"Cloning of neurotrophin defines a new subfamily of differentially			
RT	expressed neural cell adhesion molecules.";			
RL	J. Neurosci. 15:2141-2156(1995).			
CC	- FUNCTION: NEURAL CELL ADHESION MOLECULE.			
CC	- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.			
CC	- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.			
CC	- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL			
CC	SUBPLATE, AND LOWER CORTICAL LAMINAE IN THE FOREBRAIN AND IN THE			
CC	PONTINE NUCLEUS, CEREBELLAR GRANULE CELLS, AND PURKINJE CELLS IN			
CC	THE HINDBRAIN.			
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGION			
CC	SUBFAMILY.			
CC	- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U16845; AAA67445.1; -.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003598; Ig_C2.			
DR	InterPro; IPR003600; Ig_Like.			
DR	Pfam; PF00047; Ig_3.			
DR	SMART; SM00410; Ig_Like; 1.			
DR	SMART; SM00408; IgC2; 2.			
KW	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;			
KW	Repeat; Signal.			
FT	SIGNAL	1	31	POTENTIAL.
FT	CHAIN	32	321	NEUROTROPHIN.
FT	PROPEP	322	344	REMOVED IN MATURE FORM (POTENTIAL).
FT	DOMAIN	50	122	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	150	208	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	236	302	IG-LIKE C2-TYPE DOMAIN 3.


```
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE5B3B224 CRC64;
```

Query Match 90.8%; Score 1639.5; DB 1; Length 344;
Best Local Similarity 92.9%; Pred. No. 4.7e-125;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

```
QY 12 ISWAIFTGLALCLF---QGVPRVSGDATFPKAMDNTVRQGESATLRCITDNRVAV 68
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 LPWKCLVAVSLRLFLVPTGVPVRSBGATFPKAMDNTVRQGESATLRCITDNRVAV 68

QY 69 LNRSTILYAGNDKWCCLDPRVLLSNTOQYSIEIQNDVYDEGPYTCVQTDNHPKTSR 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 LNRSTILYAGNDKWCCLDPRVLLSNTOQYSIEIQNDVYDEGPYTCVQTDNHPKTSR 128

QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFSVEYLEI 188
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFSVEYLEI 188

QY 189 QGITREQSGDYECASNDVAAAPVRRVYVTVNPPYISSEAKGTGVPVGOKGTLOCEASAV 248
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 QGITREQSGDYECASNDVAAAPVRRVYVTVNPPYISSEAKGTGVPVGOKGTLOCEASAV 248

QY 249 PSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFNVSEHDYGNVTCVANSKLGHTNASI 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 PSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFNVSEHDYGNVTCVANSKLGHTNASI 308

QY 309 MLFPGAVSEVNGTSRRAGCVWLLPLVLLHLLKF 344
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 MLFPGAVSEVNGTSRRAGCVWLLPLVLLHLLKF 344
```

RESULT 2

```
CEPU_CHICK
ID CEPU_CHICK STANDARD; PRT; 353 AA.
AC Q90773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CEPU-1 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96370549; PubMed=8774445;
RA Spaltmann F., Brummendorf T.;
RT "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by
RT developing cerebellar Purkinje cells.";
RL J. Neurosci. 16:1770-1779(1996).
CC -1- FUNCTION: IT MAY BE A CELLULAR ADDRESS MOLECULE SPECIFIC TO
CC PURKINJE CELLS. IT MAY REPRESENT A RECEPTOR OR A SUBUNIT OF A
CC RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI anchor.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A MAJOR FORM AND A MINOR FORM
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: FOUND ON THE DENDRITES, SOMATA AND AXONS OF
CC DEVELOPING PURKINJE CELLS. UNDETECTABLE ON OTHER NEURONS LIKE
```

```
CC GOLGI OR GRANULE CELLS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED BY DEVELOPING CEREBELLAR PURKINJE
CC CELLS. EXPRESSION COINCIDES WITH THE GROWTH OF THE DENDRITIC TREE,
CC AFTER PURKINJE CELLS HAVE FINISHED THEIR MIGRATION FROM THE
CC VENTRICULAR ZONE (FROM E15 UNTIL E21). EXPRESSED IN THE ADULT.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
```

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DR EMBL; Z72497; CAA96578.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00408; IgC2; 2.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Alternative splicing.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 330 CEPU-1 PROTEIN.
FT PROPEP 331 353 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 48 120 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 148 206 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 234 300 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 55 113 POTENTIAL.
FT DISULFID 155 199 POTENTIAL.
FT DISULFID 241 293 POTENTIAL.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 330 330 GPI-ANCHOR (POTENTIAL).
FT VARSPIC 310 320 MISSING (IN MAJOR ISOFORM).
SQ SEQUENCE 353 AA; 38736 MW; 2550C48591EBBA6 CRC64;
```

Query Match 81.8%; Score 1477.5; DB 1; Length 353;
Best Local Similarity 78.6%; Pred. No. 5.7e-112;
Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;

```
QY 5 QPKMHSISWAIFTGLALCLFQGVPRVSGDATFPKAMDNTVRQGESATLRCITDNRVT 64
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 QAKMQHPVSWVIFAGMAALLFQGVPRVSGDATFPKAMDNTVRQGESATLRCITDNRVT 62

QY 65 RVAWLNRSTILYAGNDKWCCLDPRVLLSNTOQYSIEIQNDVYDEGPYTCVQTDNHPK 124
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 RVAWLNRSSILYAGNDKWCCLDPRVLLANTKTQYSIQIHVDVYDEGPYTCVQTDNHPK 122

QY 125 TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFSVE 184
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 TSRVHLIVQVSPKITETSSDISINEGNNISLTCIATGRPDPTTRHISPKAVGFSVE 182

QY 185 YLEIQGITREQSGDYECASNDVAAAPVRRVYVTVNPPYISSEAKGTGVPVGOKGTLOCE 244
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 YLEIQGITREQSGDYECASNDVAAAPVRRVYVTVNPPYISDAKSTGVPVGOKGILMCE 242

QY 245 ASAVPSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFNVSEHDYGNVTCVANSKLGHT 304
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 ASAVPSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFNVSEHDYGNVTCVANSKLGHT 302

QY 305 NASIMLF-----GPGAVSEVNGTSRRAGCVWLLPLVLLHLLKF 344
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 NASIMLYEETTLTPWKPGAVHDGNSGAMRSGCAMLPLAQLARQF 353
```

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RESULT 3
G55A_CHICK STANDARD; PRT; 337 AA.
ID G55A_CHICK
AC Q98892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurite inhibitor GP55-A precursor (OBCAM protein gamma isoform).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from
RL chick: structural diversity of IGLON family proteins.";
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBCAM,
RT neurotrophin, LAMP and CEPU-1.";
RL J. Cell Sci. 109:3129-3138(1996).
CC -!- FUNCTION: INHIBITS NEURITE OUTGROWTH.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
CC -!- DEVELOPMENTAL STAGE: INCREASES DURING DEVELOPMENT FROM VERY LOW
CC LEVELS AT EMBRYONIC DAY 10 AND IS MOST ABUNDANT AFTER HATCHING.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL, Y08170, CAB41420.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00408; Ig_c2; 2.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 1 317
FT PROPEP 318 337
FT DOMAIN 43 115
FT DOMAIN 143 201
FT DOMAIN 229 295
FT DISULFID 150 194
FT DISULFID 236 288
FT CARBOHYD 133 133
FT CARBOHYD 277 277
FT CARBOHYD 285 285
FT CARBOHYD 298 298
SQ SEQUENCE 337 AA; 36887 MW; BAE717551856551E CRC64;

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Query Match 72.3%; Score 1305; DB 1; Length 337;

```

Best Local Similarity 73.2%; Pred. No. 4.4e-98;
Matches 248; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 8 MHNISMAIFTGLAALCLFQGVPPVSGDATFPKAMDNTVRQGSATLRCTIDNRVTRVA 67
Dd 1 MYHPACIVFTATTALLFIPGVPPVSGDATFPKAMDNTVRQGSATLRCTIDNRVTRVA 60
QY 68 WLNRSITIIYAGNDKWCIDPRVLLSNQTQYSIEIQNVVDYDEGPTCSVQIDNHPKTSR 127
Dd 61 WLNRSITIIYAGNDKWSIDNRVILSNKTKQYSIKIHNVVDYDEGPTCSVQIDNHPKTSR 120
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTICATGRPEPTVTRHISPKAVGFSYSEDEYLE 187
Dd 121 VHLIVQVPPQIVNISSDITVNEGSSVTLMLCLAFGRPEPTVTRHLSGKGQFVSEDEYLE 180
QY 188 IQGITREQSGDYECASANDVAAPVVRKVTNVNPPYISEAKGTGVPVGQKTIQCEASA 247
Dd 181 ITGITREQSGEYECASAVNDVAAPVVRKVTNVNPPYISNAKNGASVGQKTIQCEASA 240
QY 248 VPSAEFPQWKDDKRLIEGKKGVKVENRPFSLKIFPNVSEHDYGVTCVASKLGHITNAS 307
Dd 241 VPVAEPQWFKEDTRLANGLEGVRIESKGRSLSTTFPNVSEKDYGVTCVATNKLGHITNAS 300
QY 308 IMLEFGVAVSEVSNSTSRAG--CWLPLPLVHLHLKE 344
Dd 301 IILYGPVAVHDSGNAASRAAGLCIW--ATLLARLLIDF 337

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RESULT 4
OPCM_HUMAN
ID OPCM_HUMAN STANDARD; PRT; 345 AA.
AC Q14982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opioid binding protein/cell adhesion molecule precursor (OBCAM)
DE (Opioid-binding cell adhesion molecule) (OPCML).
GN OPCML OR OBCAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Occipital cortex;
RX MEDLINE=95237612; PubMed=7721093;
RA Shark K.B., Lee N.M.;
RT "Cloning, sequencing and localization to chromosome 11 of a cDNA
RT encoding a human opioid-binding cell adhesion molecule (OBCAM).";
RL Gene 155:213-217(1995).
CC -!- FUNCTION: BINDS OPIOIDS IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY
CC INVOLVED IN CELL CONTACT.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, L34774; AAA36387.1; -.
DR MIM; 600632; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.

```

[illegible]

Query Match	70.28;	Score 1268;	DB 1;	Length 345;
Best Local Similarity	71.28;	Pred. No. 4.4e-95;		
Matches 240;	Conservative 37;	Mismatches 56;	Indels 4;	Gaps 2

[illegible]

```

RESULT      5
OPCM_BOVIN
ID          OPCM_BOVIN      STANDARD;      PRT;      345 AA.
AC          P11834;
DT          01-OCT-1989 (Rel. 12, Created)
DT          01-OCT-1989 (Rel. 12, Last sequence update)
DT          16-OCT-2001 (Rel. 40, Last annotation update)
DE          Opioid binding protein/cell adhesion molecule precursor (OBCAM)
DE          (Opioid-binding cell adhesion molecule) (OPCML).
GN          OPCML OR OBCAM OR OCAM.
OS          Bos taurus (Bovine).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC          Bovidae; Bovinae; Bos.
OX          NCBI_TaxID=9913;
RN          [1]
RP          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC          TISSUE=Brain;
RX          MEDLINE=89251576; PubMed=2721489;
RA          Schofield P.R., McFarland K.C., Hayflick J.S., Wilcox J.N.,
RA          Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H.;

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RT "Molecular characterization of a new immunoglobulin superfamily
RT protein with potential roles in oploid binding and cell contact.";
RL EMBO J. 8:489-495(1989).
CC -!- FUNCTION: BINDS OPIOIDS IN THE PRESENCE OF ACIDIC LIPIDS; PROBABLY
CC INVOLVED IN CELL CONTACT.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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DR	EMBL; X12672; CAA31192.1; -.
DR	PIR; S03199; S03199.
DR	HSSP; P01732; 1CD8.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003598; Ig_c2.
DR	InterPro; IPR003600; Ig_like.
DR	Pfam; PF00047; 1g_3.
DR	SMART; SM00410; IG_like; 1.
DR	SMART; SM00408; IGC2; 2.
KW	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	LIPID
FT	SEQUENCE
FT	PIR; S03199; S03199.
FT	HSSP; P01732; 1CD8.
FT	InterPro; IPR003006; Ig_MHC.
FT	InterPro; IPR003598; Ig_c2.
FT	InterPro; IPR003600; Ig_like.
FT	Pfam; PF00047; 1g_3.
FT	SMART; SM00410; IG_like; 1.
FT	SMART; SM00408; IGC2; 2.
FT	Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT	Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	

Query Match	70.1%;	Score 1266;	DB 1;	Length 345;
Best Local Similarity	71.6%;	Pred. No. 6.3e-95;		
Matches 240;	Conservative 34;	Mismatches 57;	Indels 4;	Gaps 2;

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QY      14 WAI FTGLAALCLF--OGV PVRSGD ATEPKAMDNVTVRQGESA TL RCTIDNRVTRVAWLN   70
        | :: || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      11 WKCLVVS LRLFLFP TGPVPVRSGDATEPKAMDNTVVRQGESATL RCTIDR VTRVAWLN   70
QY      71 RSTILYAGNDKWCLDP RVLLSNTQTQYSIEIQNV DYDEGPTCSVQT DNHPKTSRVHL   130
        | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      71 RSTILYAGNDKWSIDPRV IILNTP QYSIMIQNDVY DEGPRTCSVQT DNHPKTSRVHL   130
QY      131 IVQVSPKIVEISSDISINEGNNISLTCLATGRPREPVTWRHISPK -AVGFVSEDEYLEIQ   189
        | | | | | : | : | : | : | : | : | : | : | | | | | | | | | | | | | | | |
Db      131 IVQVPPQIMNISSDYTVABEGSSVTLTCLAI GRPREFTVWRHLSVKEGGGFVSEDEYLEIS   190
QY      190 GITREQSGDYECASANDVAAPVVRKRKYVTVNYPPIYISEAKGTGV PVGOKGITQCEASAVP   249
        | : | : | : | | | | | | | | | | : | : | : | | | | | | | | | | | | | |
Db      191 DIKRDOSGEYECSALNDVAAPDVRRKYKITVNYPPYISKAKNTGVSVGQKGIIISC EASAVP   250
QY      250 SAEFOWYKDCKRLIEGKKGVKVENRPFLSKLI FENVSEHDYGNYTCVASNKLGHTNASIM   309
        | | | | | : | | | : | : | : | : | : | | | | | | | | | | | | | | | |
Db      251 MAEFOWMEKEDTRLATGDGMRIENNGHISTLFEP NVSEKDYGYTCVATNKIGITNASIT   310
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FT	DISULFID	157	202	POTENTIAL.
FT	DISULFID	244	296	POTENTIAL.
FT	CARBOHYD	44	44	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	70	70	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	285	285	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	306	306	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	322	322	GPI-ANCHOR (POTENTIAL).
FT	VARSPPLIC	1	27	MGVCGYFLPFWKCLVAVSLRLFLVPT -> MYH4YWIWF
FT	SEQUENCE	345 AA;	38067 MW;	SATFALFETP (IN ISOFORM 2).
FT	SEQUENCE	345 AA;	38067 MW;	A3181B0753F9658E CRC64;
QY	Query Match	69.7%;	Score 1259;	DB 1; Length 345;
QY	Best Local Similarity	71.2%;	Pred. No. 2.3e-94;	
Db	Matches 240;	Conservative 34;	Mismatches 59;	Indels 4; Gaps
QY	12 ISWALFTGLALCF--QGVPYRSGDAFPKAMDNTVROGESATLRCTIDNRYTRVAV	68		
Db	9 LPWKCLVAVSLRLFLVPTGPVPRSGDAFPKAMDNTVROGESATLRCTIDRVTTRVAV	68		
QY	69 LNRSTLYAGNDKWCIDPRVVLISNTQYYSIEIONVDVDEGPYTCVQTDNHPKTSRV	128		
Db	69 LNRSTLYAGNDKWSIDPRVILVNTPTQYSIMIONVDVDEGPYTCVQTDNHPKTSRV	128		
QY	129 HLIVQYSPKIVEISSDISINEGNNISLTCTIATGRPEPTVMKHSIPK-ANGFVSEDEYLE	187		
Db	129 HLIVQYPPQIMNISSDITVNEISSVTLCLAIAGRPEPTVMKHSIPK-ANGFVSEDEYLE	188		
QY	188 IGGTREGSGDYECSSASNDVAAPVYRVRKVYVNPYPYISEAKGTGVPVGQKTLQCEASA	247		
Db	189 ISDIKRDQSGEYECSSALNDVAAPDVRRVKKITVNPYPYISKANFTGVSVGQKILSCASA	248		
QY	248 VPSAEFQWKDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYYCVASNKLGHNTAS	307		
Db	249 VPMAEQWKEKEDTRLATGLDGVRIENKGRISTLFEFNVSXKDYGNYYCVATNKLGNNTAS	308		
QY	308 IMLFGGAVSEVSNFTSRACGVMLPLVLHLHLKE	344		
Db	309 ITLYGCAVIDGVNSASRALACMLSGTFFAHFFIKF	345		
RESULT	7			
LAMP_CHICK				
AC	098919;	STANDARD;	PRT;	338 AA.
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Limbic system-associated membrane protein precursor (E19s) (CHLAMP, G19-isoform).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97157768; PubMed=9004047;			
RA	Wilson D.J.A., Kim D.S., Clarke G.A., Marshall-Clarke S., Moss D.J.;			
RT	"A family of glycoproteins (GP55), which inhibit neurite outgrowth,			
RT	are members of the Ig superfamily and are related to OBGM,			
RT	neurotrophin, LAMP and CEPV-1."			
RL	J. Cell Sci. 109:3129-3138(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97358596; PubMed=9215692;			
RA	Brummendorf T., Spaltmann F., Treubert U.;			
RT	"Cloning and characterization of a neural cell recognition molecule			
RT	on axons of the retinotectal system and spinal cord".			


```

RL Eur. J. Neurosci. 9:1105-1116(1997).
CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC PROBABLY SERVES AS A RECOGNITION MOLECULE FOR THE FORMATION OF
CC LIMBIC CONNECTIONS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y08171; CAA69357.1; -.
DR EMBL: Z94720; CAB08115.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00408; Igc2; 2.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 338 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROPEP 29 338 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 46 118 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 146 204 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 232 297 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 153 197 POTENTIAL.
FT DISULFID 239 290 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 338 AA; 37394 MW; 8FA4A60AD98426B4 CRC64;

Query Match 52.0%; Score 938.5; DB 1; Length 338;
Best Local Similarity 56.0%; Pred. No. 1.6e-68;
Matches 182; Conservative 56; Mismatches 82; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESALRCTIDNRYTRVAMLNSTILYAG 78
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 17 LRLCLLPTGLPVRSD--FTRGTDNITVRQGDALILRCFVEDRSSKVAWLNRSGIIFAG 74

QY 79 NDKWCLDPRVLLSNQTQYSIEIQNVVDYDEGPTYGSVQTDNHPKTSRVHLIVQVSPKI 138
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 75 EDKWSLDPRVELEKRSPLKYSIRIQKVDYDEGSYTCVSQTDHHPKTSQVYLIVQVPPKI 134

QY 139 VEISSDISINEGNNISLTCIATGREPPTVTRHISPKAVGFVSEDEYLEIQGITREQSGD 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 135 SNISSDITVNEGSNVLVCMANGRPDPVITWRHLPTGKEFEGEEYLEIILGITREQSGK 194

QY 199 YECASNDVAAAPVRRYKVTNPPYISAKGTGVPVGQKGTLOCEASAVPSAEFQWKD 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 195 YECKAANEVASADVKQYRVTVNPPITTESKSNEATGRQALNCEASAVPPEFEMWRD 254

QY 259 DKRLIEGRKKGVKVENRPLSKLIFENVSEHDYGNVTCVASNKLIGHTNASIMLFGGAVSE 318
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 255 DTR-INSANGLEIKSTGSQSLIMVAVNTEEHYGNVTCVAANKIGVTNASTLYTRPG-TGR 312

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QY 319 VSNGSRAGCVMLPLVLHLLK 343
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 313 VDNGSVSLAVPLMLLAASLLCLLSK 337

RESULT 8
LAMP_HUMAN STANDARD; PRT; 338 AA.
ID LAMP_HUMAN
AC Q13449;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Limbic system-associated membrane protein precursor (LSAMP).
GN LSAMP OR LAMP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96235133; PubMed=8666243;
RA Pimenta A.F., Fischer I., Levitt P.;
RT "cDNA cloning and structural analysis of the human limbic-system-
RT associated membrane protein (LAMP).";
RL Gene 170:189-195(1996).
CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
CC MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
CC OF THE HYPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON LIMBIC NEURONS AND FIBER TRACTS
CC AS WELL AS IN SINGLE LAYERS OF THE SUPERIOR COLICULUS, SPINAL
CC CHORD AND CEREBELLUM.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: U41901; AAC50569.1; -.
DR MIM: 603241; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00408; Igc2; 2.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 315 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROPEP 316 338 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 46 118 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 146 204 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 232 297 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 153 197 POTENTIAL.
FT DISULFID 239 290 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).

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DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Kilon protein precursor (Kindred of IgION).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
RX MEDLINE=99175207; PubMed=10075727;
RA Funatsu N., Miyata S., Kumanooh H., Shigeta M., Hamada K., Endo Y.,
RA Sokawa Y., Maekawa S.;
RT "Characterization of a novel rat brain glycosylphosphatidylinositol-
RT anchored protein (Kilon), a member of the IgION cell adhesion molecule
RT family.";
RL J. Biol. Chem. 274:8224-8230(1999).
CC -!- FUNCTION: CELL-ADHESION (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: AB017139; BAA75649.1; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00408; IgC2; 2.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 31
FT CHAIN 32 ? KILON PROTEIN.
FT PROPEP 348 ? REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 47 119 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 147 204 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 232 300 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 54 112 POTENTIAL.
FT DISULFID 154 197 POTENTIAL.
FT DISULFID 239 291 POTENTIAL.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 348 AA; 37858 MW; 37E90D1C7D24ACAB CRC64;

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Query Match 45.1%; Score 815; DB 1; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.5e-58;
Matches 160; Conservative 66; Mismatches 101; Indels 10; Gaps 5;

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QY 11 SISW-AFTGLALCLFQGVPRSGDATFP-KAMDNTVRQGESATLRCTIDNRVTRVA 67
DQ 11 SNQMLAAVLLSLCS-CLPAGQSV-----DFPMAAVDNMLVRKGDPTAVLRKYIEDGASKGA 64
DQ 68 WLNRSITIVAGNDKWCIDPRVLLSNTQTQYSIEIQNVVDVDEGPTVCSVQTDNHPKTSR 127
DQ 65 WLNRSITIFAGGDKWSDVPRVSIPTLNKRDYSIQNVVDVDEGPTVCSVQTDNHPKTSR 124
QY 128 VHLIVQVSPKIVEISDSINEGNISLTCTIATGRPEPTVTRHISPKAVGVSSEDEYLE 187
DQ 125 VHLTVQVPPKIYDISMDTINEGNVTITCTIATGKPEPAISWRHISPSAKPF-ENGQYLD 183

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QY 188 IQGTRQSGDYECSASNDVAAPVRRKVTYNNPPYISAKGTGVPVGKGTLCQCEASA 247
DQ 184 IYGTIRDQAGEYECSAENDVSFPDYKKVRVYVNFAPTIQETKSGTVTPGSGLICREAG 243
QY 248 VPSAEFQWYKDKRLIEGKKGVKVENRPLSKLIFENVSEHDYGNVTCVSNKLGHTNAS 307
DQ 244 VPPPAFEWYKGEKRLFNQGGQGITIQNFSTRSLITVTNTQEHFGNYTCVANKLGTNAS 303
QY 308 IMLEPGAVSEVSNGTSRRAGCVWLLPLVLHLIKE 344
DQ 304 LPLNPSTAQYGTGSACDLFSCWSLALTTSVISIF 340

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RESULT 11
AMAL_DROME STANDARD; PRT; 333 AA.
ID AMAL_DROME
AC P15364; Q9V3A5;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 01-MAR-2002 (Rel. 41, last annotation update)
DE Amalgam protein precursor.
GN AMA OR BG:DS00276.6 OR CG2198.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=89028670; PubMed=3141062;
RA Seeger M.A., Haffley L., Kaufman T.C.;
RT "Characterization of amalgam: a member of the immunoglobulin
RT superfamily from Drosophila.";
RL Cell 55:589-600(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA Palazzolo M.J.;
RT "Complete sequence of the Antennapedia complex of Drosophila.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

```


RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: M23561; AAA28367.1; -.
DR EMBL: AE001572; AAD19797.1; -.
DR EMBL: AE003674; AAF54084.1; -.
DR EMBL: AY051911; AAK93335.1; -.
DR PIR: A31923; A31923.
DR FlyBase; FBgn0000071; Ama.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00408; IgC2; 2.
KW Immunoglobulin domain; Glycoprotein; GPI-anchor; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 ? AMALGAM PROTEIN.
FT PROPEP ? 333 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 127 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 154 215 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 244 314 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFID 46 117 PROBABLE.
FT DISULFID 161 208 PROBABLE.
FT DISULFID 251 307 PROBABLE.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 83 83 Q -> K (IN REF. 1).
SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match 16.5%; Score 297.5; DB 1; Length 333;
Best Local Similarity 29.7%; Pred. No. 7.9e-17;
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

QY 44 NNTVROGESATLRCITDN-RVYRVAVMLNR-----STIIYAGNDKWCIDPR--VVLISN 93
DB 33 DVVASVGDVSVEENCTVEEVGQLSVSWAKRSESDTNSVYLSMRNITSLDQRYNVTYIEG 92
QY 94 TQFQ---YSIEIQNVVDYDEGPTCTSVQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148

DB 93 PRGSAIYTRFRQNIENVSDMPYECQVLYSATEKVTYTKISLQIKTPPIAENTPKSLVT 152
QY 149 EGNISLTCIATGRPEPTVWRH---ISPKAVGFVSEDEYLEIQTREQSGDYECSSAS 204
DB 153 EGONLELTCHANGFPKPTISWARENHNAVP-AGHLLAEPFLRIRSVHRMDRGYICIAQ 211
QY 205 NDVAAPVRRYKVTNYPYIS-EAKGTGVPVGQKGTIQCESAASAVPSAEFQWKDKRLI 263
DB 212 NEQGQPKRLIRVEVEFRPQIAVQRPKIAQWVSHSAELSCSVQGYPAFTVWHKNGVPL- 270
QY 264 EGKKGKVENR-----PFLSKLIFNVSEHDYGNVTCVASNKLGHTNASIMLF 311
DB 271 QSSRHHVANTASSSGTTTSYLRIIDSVGEDEFGDYCCNATNKLGHADARLHLF 323
RESULT 12
ID NCA2_MOUSE STANDARD; PRT; 725 AA.
AC P13594; Q61950;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neural cell adhesion molecule, phosphatidylinositol-linked isoform
DE precursor (N-CAM 120) (NCAM-120).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=87246524; PubMed=3595563;
RA Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
RA Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT a Mr 79,000 polypeptide without a membrane-spanning region.";
RL EMBO J. 6:907-914(1987).
RN [2]
RP SEQUENCE OF 20-700 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=89251563; PubMed=2721486;
RA Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT "Differential exon usage involving an unusual splicing mechanism
RT generates at least eight types of NCAM cDNA in mouse brain.";
RL EMBO J. 8:385-392(1989).
RN [3]
RP SEQUENCE OF 642-725 FROM N.A.
RX MEDLINE=88283628; PubMed=3396534;
RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT "Differential splicing and alternative polyadenylation generates
RT distinct NCAM transcripts and proteins in the mouse.";
RL EMBO J. 7:625-632(1988).
RN [4]
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=3512556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
RT domain of mammalian neural cell adhesion molecules.";
RL J. Biol. Chem. 261:3396-3401(1986).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE IIT-LIKE DOMAINS.
CC -----
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DR	EMBL; X07200; CA30177.1; -.			
DR	EMBL; Y00051; -: NOT_ANNOTATED_CDS.			
DR	EMBL; X06328; CA329641.1; -.			
DR	EMBL; X07195; CA30173.1; -.			
DR	EMBL; X07244; CA30230.1; -.			
DR	EMBL; X15051; CA33150.1; -.			
DR	EMBL; X15052; CA33151.1; -.			
DR	PIR; A29673; JMSNL.			
DR	MGI; MGI:97281; Ncam.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF00041; fn3; 2.			
DR	Pfam; PF00047; Ig; 5.			
DR	SMART; SM00060; FN3; 2.			
DR	SMART; SM00408; IGC2; 5.			
KM	Cell adhesion; Glycoprotein; Transmembrane; Repeat;			
KW	Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.			
FT	SIGNAL	1	19	
FT	CHAIN	20	1115	
FT				NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM.
FT	DOMAIN	20	711	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	712	729	POTENTIAL.
FT	DOMAIN	730	1115	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	34	103	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	132	196	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	228	295	IG-LIKE C2-TYPE DOMAIN 3.
FT	DOMAIN	323	393	IG-LIKE C2-TYPE DOMAIN 4.
FT	DOMAIN	420	487	IG-LIKE C2-TYPE DOMAIN 5.
FT	DOMAIN	519	596	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	625	692	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	152	156	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	161	165	HEPARIN-BINDING (POTENTIAL).
FT	DISULFID	41	96	PROBABLE.
FT	DISULFID	139	189	PROBABLE.
FT	DISULFID	235	288	PROBABLE.
FT	DISULFID	330	386	PROBABLE.
FT	DISULFID	427	480	PROBABLE.
FT	CARBOHYD	222	222	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316	316	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	348	348	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	424	424	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	479	479	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	810	1076	MISSING (IN ISOFORM N-CAM 140).
SO	SEQUENCE	1115 AA;	119351 MW;	2C93DCD474CFBCAF CRC64:

Query Match	15.7%;	Score 283.5;	DB 1;	Length 1115;
Best Local Similarity	25.8%;	Pred. No. 5.4e-15;		
Matches 75;	Conservative 45;	Mismatches 130;	Indels 41;	Gaps 7

OY	44	NVTVRQGSATLRCRTIDNRVTRVAMINRSTILYAGNDKWCLEPRVV-----LLSNIQ	95
		: :	:
Dd	222	NATANLGOSVTLVCADG-----FPEPTM-----SWTKDGEPIENEEDERSRSVS	268
		: :	:
OY	96	TQYSIEIONVDVDEGGPYTCGVCFDNHFKTSRVHLIVQSPKIVEISSDISINEGNISL	155
		: : : :	: : : : : :

[illegible]

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RESULT 14
NCAL_CHICK
ID NCAL_CHICK STANDARD: PRT; 1091 AA.
AC P13590; Q90919; Q90918;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neural cell adhesion molecule, large isoform precursor (N-CAM 180)
DE [Contains: N-CAM 140].
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianina
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE OF 1-175 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87206190; PubMed=3576199;
RA Cunningham B.A., Hemperly J.J., Murray B.A., Prediger E.A.,
RA Brackenbury R., Edelman G.M.;
RT "Neural cell adhesion molecule: structure, immunoglobulin-like
RT domains, cell surface modulation, and alternative RNA splicing.";
RL Science 236:799-806(1987).
RN [2]
RP SEQUENCE OF 128-1091 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=86206089; PubMed=3458261;
RA Hemperly J.J., Murray B.A., Edelman G.M., Cunningham B.A.;
RT "Sequence of a cDNA clone encoding the polysialic acid-rich and
RT cytoplasmic domains of the neural cell adhesion molecule N-CAM.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3037-3041(1986).
RN [3]
RP SEQUENCE FROM N.A. (726 AA FORM).
RX MEDLINE=87092340; PubMed=3467341;
RA Hemperly J.J., Edelman G.M., Cunningham B.A.;
RT "cDNA clones of the neural cell adhesion molecule (N-CAM) lacking a
RT membrane-spanning region consistent with evidence for membrane
RT attachment via a phosphatidylinositol intermediate.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9822-9826(1986).
RN [4]
RP SEQUENCE OF 810-1069 FROM N.A.
RX MEDLINE=87033934; PubMed=3771645;
RA Murray B.A., Owens G.C., Prediger E.A., Crossin K.L.,
RA Cunningham B.A., Edelman G.M.;
RT "Cell surface modulation of the neural cell adhesion molecule
RT resulting from alternative mRNA splicing in a tissue-specific
RT developmental sequence.";
RL J. Cell Biol. 103:1431-1439(1986).
RN [5]
RP SEQUENCE OF 1-17 FROM N.A.
RX MEDLINE=93122797; PubMed=1478668;
RA Colwell G., Li B., Forrest D., Brackenbury R.;
RT "Conserved regulatory elements in the promoter region of the N-CAM
RT gene.";
RL Genomics 14:875-882(1992).
RN [6]
RP SEQUENCE OF 1-17 FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Erythrocyte;
RA Sasner M., Covault J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 12, 2002, 00:33:42 ; Search time 133.38 Seconds

(without alignments)
446.171 Million cell updates/sec

Title: US-09-700-397-3
Perfect score: 1806
Sequence: 1 MKTIQPKMHNISISWAFITGL.....RRAGCVLLPLVLHLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1665.5	92.2	344	4 Q9P121	Q9P121 homo sapien
2	1616.5	89.5	344	11 Q99PJ0	Q99PJ0 mus musculu
3	1428	79.1	313	13 Q57596	Q57596 gallus gall
4	1427.5	79.0	344	13 Q93242	Q93242 gallus gall
5	1357.5	75.2	315	13 Q9DGI5	Q9DGI5 gallus gall
6	1275.5	70.6	344	13 Q9DF61	Q9DF61 gallus gall
7	946	52.4	334	7 Q02870	Q02870 gallus gall
8	930.5	51.5	350	7 Q02869	Q02869 gallus gall
9	842	46.6	352	13 Q9W6V2	Q9W6V2 gallus gall
10	599	33.2	261	13 Q9W6V1	Q9W6V1 gallus gall
11	338.5	18.7	413	5 Q9VAR6	Q9VAR6 drosophila
12	333	18.4	315	5 Q9VMB2	Q9VMB2 drosophila
13	308.5	17.1	528	5 P91670	P91670 drosophila
14	306	16.9	545	5 Q9VCT4	Q9VCT4 drosophila
15	290.5	16.1	2673	4 Q96SC3	Q96SC3 homo sapien
16	290.5	16.1	5636	4 Q96RW7	Q96RW7 homo sapien

17	287	15.9	846	13 Q57577	Q57577 cynops pyr
18	287	15.9	1100	13 Q57576	Q57576 cynops pyr
19	285.5	15.8	603	5 Q9NKF5	Q9NKF5 drosophila
20	284.5	15.8	607	5 Q9VP08	Q9VP08 drosophila
21	282.5	15.6	605	11 Q921P2	Q921P2 mus musculu
22	279.5	15.5	725	13 Q73633	Q73633 xenopus lae
23	278.5	15.4	4162	13 Q98918	Q98918 gallus gall
24	273.5	15.1	725	13 Q73634	Q73634 xenopus lae
25	272.5	15.1	1323	13 Q08476	Q08476 gallus gall
26	269.5	14.9	484	5 Q26475	Q26475 schistocerc
27	268.5	14.9	1496	4 Q92626	Q92626 homo sapien
28	265	14.7	1482	5 Q9V4Y0	Q9V4Y0 drosophila
29	261	14.5	1031	13 Q90YM2	Q90YM2 brachydanio
30	261	14.5	1395	5 Q44924	Q44924 drosophila
31	260.5	14.4	496	5 Q9W260	Q9W260 drosophila
32	260.5	14.4	500	5 Q9XZB7	Q9XZB7 drosophila
33	260.5	14.4	500	5 Q961W0	Q961W0 drosophila
34	260	14.4	604	4 Q96CJ3	Q96CJ3 homo sapien
35	260	14.4	1395	5 Q9W213	Q9W213 drosophila
36	259	14.3	7962	4 Q10465	Q10465 homo sapien
37	255.5	14.1	838	13 Q90YM1	Q90YM1 brachydanio
38	255	14.1	359	5 Q9V6C2	Q9V6C2 drosophila
39	254.5	14.1	5198	5 Q76518	Q76518 caenorhabdi
40	250.5	13.9	885	5 Q9VPZ6	Q9VPZ6 drosophila
41	250.5	13.9	1342	5 Q9GPP6	Q9GPP6 drosophila
42	250	13.8	795	13 Q90YM0	Q90YM0 brachydanio
43	248	13.7	467	5 Q9VMN7	Q9VMN7 drosophila
44	245.5	13.6	1065	4 Q94898	Q94898 homo sapien
45	244.5	13.5	512	4 Q96DN8	Q96DN8 homo sapien

ALIGNMENTS

RESULT 1
Q9P121 PRELIMINARY; PRT; 344 AA.
ID Q9P121
AC Q9P121;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEUROTIRMIN.
GN HNT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF126426; AAR37591.1; -
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00408; IgC2; 2.
DR SMART: SM00410; Ig_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;

Query Match 92.2%; Score 1665.5; DB 4; Length 344;
Best Local Similarity 95.2%; Pred. No. 7.4e-138;
Matches 320; Conservative 3; Mismatches 10; Indels 3; Gaps 1;

QY 12 ISNAFTGLAALCLF--QGVVRSQDAPPKAMDNVTVRQGESATLRCTIDNRVTRVAV 68
Db 9 LPWACLVVSVSLRLFLVPTGVPRSGDAPPKAMDNVTVRQGESATLRCTIDNRVTRVAV 68
QY 69 LNRSTLYAGNDKWCILDPRVYLLSNQTOYSIEIQNVVDYDEGPTCSYQTDNHPKTSRY 128
|||||

Db 69 LNKSTILYAGNDKWCCLDPVVLNSMTQOYSIEIQNDVYDEGPYTCVQTDNHPKTSRV 128

QY 129 HLIVQVSPKIVEISSDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
|||||

Db 129 HLIVQVSPKIVEISSDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEI 188

QY 189 QGITREQSGDYECSSASNDYAAPVVRKYVTVNYPPYISEAKGTGPVGOKGTLOCEASAV 248
|||||

Db 189 QGITREQSGDYECSSASNDYAAPVVRKYVTVNYPPYISEAKGTGPVGOKGTLOCEASAV 248

QY 249 PSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFENVSEHDYGNVTCVASNKLIGHTNAST 308
|||||

Db 249 PSAEFQWYKDDKRLIEGKKGVKVENRPLSKLIFENVSEHDYGNVTCVASNKLIGHTNAST 308

QY 309 MLEFGPQAVSEVSNGTSRRAGCVWLLPLVLHLHLAKF 344
|||||

Db 309 MLEFGPQAVSEVSNGTSRRAGCVWLLPLVLHLHLAKF 344

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RESULT 2
Q99PJ0
ID Q99PJ0 PRELIMINARY; PRT; 344 AA.
AC Q99PJ0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEUROTIRMIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=BRAIN;
RA. Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
RT "Cloning and expression of mouse neurotirlin gene in the developing
RT nervous system.";
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF282980; AAK00276.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; IgC2; 3.
DR SMART; SM00410; Ig_like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA: 37924 MW: 3ECC6D5EE6C5C17D CRC64:

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[illegible]

Db 249 PSAHEQWEKDKRLVEGKKGVKENRPELSKLTFFENVSEHDYGYNTCVASNKRLGHTNASI 308

QY 309 MLEFGPQAVSEVSNGTSSRACGWWLLPLVLHLLEK 344
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309 MLEFGPQAVSEVSNGTSSRACIWWLLPLVLHLLEK 344

Db

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RESULT      3
057596
ID 057596          PRELIMINARY;          PRT;          313 AA.
AC 057596;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEURAL SECRETED GLYCOPROTEIN (CEPU-SE ALPHA 2 ISOFORM).
GN CEPU OR CEPU-SE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim D., Moss D.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT "Characterisation of CEPU-Se, a secreted isoform of the IgION family
RT protein CEPU-1.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ225897; CAA12649.1; -
DR EMBL; AF292935; AAG01878.1; -
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 2.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 313 AA; 34482 MW; 99AD825CAEA4A5347 CRC64;

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[illegible]

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RESULT 4
O93242 ID 093242 PRELIMINARY; PRT; 344 AA.
AC 093242;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CEPU-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RT "CEPU-1: an Immunoglobulin Superfamily Molecule, Has Cell Adhesion
RT Activity and Shows Dynamic Expression Patterns in Chick Embryonic
RT Spinal Cord.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011810; BAA31514.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR SMART; SM00410; Ig_like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA; 37613 MW; 22CAA8F526A6B57E CRC64;

Query Match 79.0%; Score 1427.5; DB 13; Length 344;
Best Local Similarity 79.2%; Pred. No. 5.5e-117;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

OY 11 SISNAIFGTGLALCLF--QGVPVRSGDATFPKAMDNTVVRQGESATLRCITIDNRVRYA 67
Db 8 ALPWRCLVLCRLFLVLPAGVPRSGDATFPKAMDNTVVRQGESATLRCISVDNRVRYA 67
OY 68 WLNKSTILYAGNDKWCCLDPRVVLLSNTQTSIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
Db 68 WLNKSSILYAGNDKWCCLDPRVVLLANTKTQYSIQIHVDVYDEGPTCSVQTDNHPKTSR 127
OY 128 VHLIVQVSPKIVEISSDISINEGNNISLTGCIATGRPEPTVWRHISPKAVGFSEDEYLE 187
Db 128 VHLIVQVSPKITEISSDISINEGNNISLTGCIATGRPDPTITWRHISPKAVGFISEDEYLE 187
OY 188 IQGITREQSGDYECASANDVAAPVRRVKVTWNPYPISEAKGTGVPYGQKGLTQCEASA 247
Db 188 ITGITREQSGEYECASANDVAAPVQRVKVTWNPYPISDAKSTGVPYGQKGLTMCESASA 247
OY 248 VPSAEFQWKDKKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNAS 307
Db 248 VPSADFQWKDKKRLAEGQKGLKVENKAFPSRLTFFNVSQDYGNTCVASNQGLGNTNAS 307
OY 308 IMLEFGAVSEVNGTSRRAGCVWLLPLVLHLLKF 344
Db 308 MIIYGPNAVHDCNSGAWRRGSCAWLLALPLAQLARQF 344

RESULT 5
O9DG15 ID 09DG15 PRELIMINARY; PRT; 315 AA.
AC 09DG15;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CEPU-SE ALPHA 1 ISOFORM.
GN CEPU-SE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
```

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT "Characterisation of CEPU-Se, a secreted isoform of the IGLON family
RT protein CEPU-1.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292936; AAG01879.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IgC2; 3.
DR SMART; SM00410; Ig_like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 315 AA; 34606 MW; 68C5D27F0DDC6FB2 CRC64;
```

```
Query Match 75.2%; Score 1357.5; DB 13; Length 315;
Best Local Similarity 83.0%; Pred. No. 6.7e-111;
Matches 253; Conservative 26; Mismatches 23; Indels 3; Gaps 1;
```

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OY 11 SISNAIFGTGLALCLF--QGVPVRSGDATFPKAMDNTVVRQGESATLRCITIDNRVRYA 67
Db 8 ALPWRCLVLCRLFLVLPAGVPRSGDATFPKAMDNTVVRQGESATLRCISVDNRVRYA 67
OY 68 WLNKSTILYAGNDKWCCLDPRVVLLSNTQTSIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
Db 68 WLNKSSILYAGNDKWCCLDPRVVLLANTKTQYSIQIHVDVYDEGPTCSVQTDNHPKTSR 127
OY 128 VHLIVQVSPKIVEISSDISINEGNNISLTGCIATGRPEPTVWRHISPKAVGFSEDEYLE 187
Db 128 VHLIVQVSPKITEISSDISINEGNNISLTGCIATGRPDPTITWRHISPKAVGFISEDEYLE 187
OY 188 IQGITREQSGDYECASANDVAAPVRRVKVTWNPYPISEAKGTGVPYGQKGLTQCEASA 247
Db 188 ITGITREQSGEYECASANDVAAPVQRVKVTWNPYPISDAKSTGVPYGQKGLTMCESASA 247
OY 248 VPSAEFQWKDKKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNAS 307
Db 248 VPSADFQWKDKKRLAEGQKGLKVENKAFPSRLTFFNVSQDYGNTCVASNQGLGNTNAS 307
OY 308 IMLEFG 312
Db 308 MIIYG 312
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RESULT 6
O9DF61 ID 09DF61 PRELIMINARY; PRT; 344 AA.
AC 09DF61;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OBCAM ALPHA 1 ISOFORM.
GN OBCAM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20499204; Pubmed=11042360;
RA Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;
RT "Co-localisation, heterophilic interactions and regulated expression
RT of IGLON family proteins in the chick nervous system.";
RL Brain Res. Mol. Brain Res. 82:84-94(2000).
DR EMBL; AF292934; AAG01877.1; -.
```


DR InterPro; IPR003559; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00410; Ig_like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 344 AA; 37531 MW; 37FE6051CBFE0E7B4 CRC64;

Query Match	70.6%;	Score 1275.5;	DB 13;	Length 344;
Best Local Similarity	72.8%;	Pred. No. 1.2e-103;		
Matches 246;	Conservative 32;	Mismatches 53;	Indels 7;	Gaps 3;

QY	12	ISWAIFTGIALCLF--QGVPVRSGDATEPKAMNVTVRQGESATLRCTIDNRVTRVAM	68
Dd	9	LPMRCLVAVLCRLLFVPAVGVPVRSGDATEPKAMNVTVRQGESATLRCTVDPRVRVAM	68
QY	69	LNKSTIIAAGNDKMCDLBRVLLSMTQTQYSIEIONVDVYDEGPYTCSVQTDNHHPKTSRV	128
Dd	69	LNKSTIIAAGNDKWSIDNRVILSNMKTQYSIKIHNVDVYDEGPYTCSVQTDNHHPKTSRV	128
QY	129	HLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVWRHISPKAVFVSEDEYLEI	188
Dd	129	HLIVQVPPIVNISSDTITVNEGSSVTLMLCFLAGREPTVTRHLSGKGQGFVSEDEYLEI	188
QY	189	QGITERQSGDYECSASNDVAAPVVRKYTVTNVPEYISEAKGTGVPVGOKGTLOCEASAV	248
Dd	189	TGITREGOSEYECSAVNDVAAPVPRKYKVTVTNVPEYISNAKNIGASVGOKEITIOCEASAV	248
QY	249	PSAEFQWYKKDDKRLLIEGGKKGVKENBPFLSKLIFFNVSEHDYCNITCVASNKLGHNTNASI	308
Dd	249	PVAEFQWEKEDTRLANGLIEGVRIESKGRSLTLEFFNVSEKDYGNITCVAINKLGNTNASI	308
QY	309	MLFGPGAVSEVSNGTSRRAG--CWULLPLVLVHLHLKF	344
Dd	309	ILYGPAGVAHDSGNAASRAAGLCIW--ATLLARLIDF	344

RESULT	7
ID	002870
AC	002870;
DT	01-JUL-1997 (TREMblrel. 04, Created)
DT	01-JUL-1997 (TREMblrel. 04, last sequence update)
DT	01-DEC-2001 (TREMblrel. 19, last annotation update)
DE	CHLAMP, G9-ISOFORM PRECURSOR.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE=97358596; PubMed=9215692;
RT	Brennendorf T., Spaltmann F., Treubert U.;
RT	"Cloning and characterization of a neural cell recognition molecule on
RL	axons of the retinotectal system and spinal cord.";
DR	Eur. J. Neurosci. 9:1105-1116(1997).
DR	EMBL; Z94718; CAB08113.1; -.
DR	InterPro; IPR003598; Ig_C2.
DR	InterPro; IPR003600; Ig_like.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig_3.
DR	SMART; SM00408; IGc2; 2.
DR	SMART; SM00410; IG_like; 1.
KW	Brain; GPI-anchor; Immunoglobulin domain; Signal.
KW	SIGNAL
FT	CHAIN
SO	SEQUENCE
334 AA:	37288 MW; DB4OA768D9609E77 CRC64;

Query Match	52.4%;	Score 946;	DB 7;	Length 334;
Best Local Similarity	55.2%;	Pred. No. 8.9e-75;		
Matches 182;	Conservative 57;	Mismatches 85;	Indels 6;	Gaps 4;

[illegible]

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RESULT      8
002869
ID      C02869      PRELIMINARY;      PRT;      350 AA.
AC      002869;
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DT      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      CHLAMP, G11-ISOFORM PRECURSOR.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BRAIN;
RX      MEDLINE=97358596; PubMed=9215692;
RA      Bruemendorf T., Spaltmann F., Treubert U.;
RT      "Cloning and characterization of a neural cell recognition molecule on
RT      axons of the retinotectal system and spinal cord.";
RL      Eur. J. Neurosci. 9:1105-1116(1997).
DR      EMBL; Z94719; CAB08114.1; -.
DR      InterPro: IPR003598; Ig_c2.
DR      InterPro: IPR003600; Ig_like.
DR      InterPro: IPR003006; Ig_MHC.
DR      Pfam; PF00047; Ig_3.
DR      SMART; SM00408; IgC2; 2.
DR      SMART; SM00410; Ig_like; 1.
KW      Brain; GPI-anchor; Immunoglobulin domain; Signal.
FT      SIGNAL      1      28      POTENTIAL.
FT      CHAIN      29      350      CHLAMP, G11-ISOFORM.
SQ      SEQUENCE      350 AA: 38656 MW: 0844892878894D4 CRC64:

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	Query Match	51.5%;	Score 930.5;	DB 7;	Length 350;
	Best Local Similarity	54.3%;	Pred. No. 2.2e-73;		
	Matches 183; Conservative	56;	Mismatches 81;	Indels 17;	Gaps 5;
QY	20 LALCLF-QGVPRVSGDATFPKAMDNYTVRQGESATLRCTIDNRYTRVAMLNRSIIYAG	78			
	: : : : : : ::				
Db	17 LRLLCLPTGLPVRSD--FTRTGDNITVRQGDPAILRCFEVEDRSSKVAMLNRSGLIFAG	74			

QY	79	NDKKCLDPRVLLSNTQTOYSIEIONVDVYDEGPYCSVQTDNHEKTSRVHLIVQVSPKI	138
		: : : : : :	
Db	75	EDKMSLDPRVELEKRSPLXSLRIQKVYDEGSYCSVQTOHHKTSQVYLIVQVPPKI	134
QY	139	VEISSDISINEGNNSIATCIATGRPEPTVWRHISPKAVGVSEDEYLEIQGITREQSGD	198
		: : : : : :	
Db	135	SNISSDITVNGESNVTIJCANGRPEPYITWRHLTPTGKEFEDEEYLEITGITREQSGK	194
QY	199	YECASASNDVAAPVVRRAKYTVNYPPTISEAKGTGVYGOKGITQCEASAVPSAEFOWYKD	258
		: : : : : : : : : : : : : : : : : : :	
Db	195	YECKAANEVASADVKQVARTVNYPTITESKSNEATGRQALLRCEASAVPPDFEWYRD	254
QY	259	DKRLIEGKKGVKENRPFSLKLIFENVSEHDYGANTCVASNKLGHTNASIMLF-----	311
		: : : : : : : : : : : : :	
Db	255	DTR-INSANGLLEIKSTGSOGLMVAANTVEHYGNTCVAAANKLGVTNASLYKRVLP TL	313
QY	312	-----GPGAVSEVSNSTSRRAQCVWLIPLVLLHLIK	343
		: : : : : : : :	
Db	314	FNPFPGPQ--TGRVNDGVSVAIPLWLLAASLTCLTSK	349

RESULT	9	
Q9W6V2		
ID	Q9W6V2	PRELIMINARY;
AC	Q9W6V2;	PRT; 352 AA.
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	NEUROTACTIN-L.	
GN	NTRA-L.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae	
OC	Gallus	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN;	
RA	Bruemendorf T.;	
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	

RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99264333; PubMed=10330412;
RA Mary A., Sirim P., Spaltmann F., Piaggge A., Kauselmann G., Buck F.
RA Rathjen F.G., Brummendorf T.;
RT "Neurotactin, A novel neutrite outgrowth-promoting Ig-like protein
RT that interacts with CEPU-1 and LAMP.";
RL J. Cell Biol. 145:865-876(1999).
DR EMBL; AJ132999; CAB44446.1; -.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 2.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 352 AA; 37944 MW; B0FA99F295FD8FA0 CRC64;

Query Match	46.6%;	Score 842;	DB 13;	Length 352;
Best Local Similarity	48.08;	Pred. No. 1.3e-65;		
Matches 159;	Conservative 68;	Mismatches 102;	Indels 2;	Gaps 2

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QY 11 SISWAIFGTALALCLFQGVVVRSGDATEP-KAMDNVTVRQGESATLRCTIDNRYTVAML 69
    | 1 | | | : : | | | : : | | | : : | |
Db 11 SHOWLAVALLGLCCLLPAGRLAAPGDFPGAADSLVVRKGDYAVLRCLYLEDGASKGAWL 70
QY 70 NRSTILVAGNDKWCILDBRVVLLSNTOQYISIEIQANDVYDEGPYTCVSQOTDNHPKTSRVH 129
    | | | : : | | | : | | | : : | | | : | | | : | | | : | | | : | |
Db 71 NRSSTILFAGSDKMSVDPKRSIATANKREYSLQIQVDVYTDIDGPYTCVSQOTQHPRTMQVH 130
QY 130 LIVQVSPKIVEISSDISINEGNNSILCLCIATGREPPTVTRHRHSPKAVGFAVEDEYLEIQ 189

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Db      131 LTVQVSPKIFRISDDIVNVEGNSVTLVCLATGKPEDISMRHISPAKFES-QGYLDIY 189
QY      190 GITREQSGDYECSSANDVAAPVVRRAKVTYVNPPIYISEAKGTGPVGQGTIQCEASAVP 249
Db      190 GTRDQAGEYECEASANDVASPDYKVKVATVNFAPITQELKSSGWLGGNGLIRCEGAGVP 249
QY      250 SAEFQWYKDKRLIEGKKGVENRPLSKLIFENVSEHDYGNTCVYASNKIIGHTNASIM 309
Db      250 APFVEWYRGERKLISGQGGITIKNYSIRSLLTVTINVTBEHFGNYTCVAANKIGMTNASLP 309
QY      310 LFGPGAVSEVSNGTSRRAGCWLLPLVLVHL 340
Db      310 LNPSTAQYGITGDAEVLFEFCWYLVLTLSL 340

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RESULT	10		
Q9W6V1			
ID	Q9W6V1	PRELIMINARY;	PRT; 261 AA.
AC	Q9W6V1;		
DT	01-NOV-1999	(TREMBLrel. 12, Created)	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	NEUROTRACTIN-S.		
GN	NTFA-S.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Bruemendorf T.;		
RL	Submitted (MAR-1999)	to the EMBL/GenBank/DBJ databases.	
RT			

RP SEQUENCE FROM N.A.
RA MEDLINE=99264333; PubMed=10330412;
RX Marg A., Strim P., Speltmann F., Plagege A., Kauselmann G., Buck F.,
RA Rathjen F.G., Brummendorf T.;
RT "Neurotracclin, A novel neurite outgrowth-promoting Ig-like protein
RT that interacts with CEPV-1 and LAMP.";
RL J. Cell Biol. 145:865-876(1999).
DR EMBL; AJ132998; CAB44445.1; -
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 261 AA; 28205 MW; 80E74DFA658802F3 CRC64;

Query Match	33.2%;	Score 599;	DB 13;	Length 261;
Best Local Similarity	52.6%;	Pred. No. 1.7e-44;		
Matches 112;	Conservative 45;	Mismatches 54;	Indels 2;	Gaps 2;

[illegible]

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RESULT 11
Q9VAR6 PRELIMINARY; PRT; 413 AA.
ID Q9VAR6;
AC Q9VAR6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CG14521 PROTEIN (GH08175P).
GN CG14521.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003767; AAF56835.1; -
DR EMBL; AY060653; AAL28201.1; -
DR FlyBase; FBgn0039617; CG14521.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
RA Pfam; PF00047; Ig_3.
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DR SMART; SM00408; Ig_c2; 2.
DR SMART; SM00410; Ig_1like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 413 AA; 45291 MW; ECOD9A20F7AE0255 CRC64;

Query Match
Best local Similarity 18.7%; Score 338.5; DB 5; Length 413;
Matches 103; Conservative 55; Mismatches 147; Indels 63; Gaps 13;

QY 35 DATEPKAMDNVTRQGESATLRCITDN-RVTRVAVLNRG--TILYAGNDKWLDPVVL 91
DB 38 DPEFIGFINNVTPAGREALLACSVRNLCNNKVGWLRASDQTLVALQGRVVTNHRISVM 97
QY 92 SNTQTQYSLIQNVVDYDEGPYTCVQTDNHPKTSRVHLI-VQVSPKIV--EISSDISIN 148
DB 98 HODMHTWKLIKSLKRESDRCCYMCQINTS--PMKKQVCIDVQVPPDITNESSADLAVQ 155
QY 149 EGNMISLTCIATGRPEPTVWRH-----ISPKAVGVSEDEY----LEIGITREQS 196
DB 156 EGEDATLTCAKATGNPQPRVTRREDGEMILLRKPGSRELKVESYNGSSLRLRLERRQM 215
QY 197 GDYECASANDVAAPVRYKVTNYPPIYI-SEAKGTGVPVQKGTLQCEASAVPSAEFQW 255
DB 216 GAYLCIASNDVPPAVSKRVSLSVGFAPVWRAPSQGLGTPLGSDVQLEQVEASPSVSYW 275
QY 256 YK-----DCKRLIEGKKGVKVENRP--FLSKLIFNVSEHDYG 291
DB 276 LKGARTSNGEASVSTASLESQSGPEMLLDGPKYGTERRDGYRGVWLLVRSFSDVG 335
QY 292 NYTCVASNKLIGHTNASIMLF---GPGA-----VSEVSNGTSRRAGCVWLLP 334
DB 336 TYHCVSTNLGRAEGTLRLYEIKLHFGASASNDHLNLYIGGLEEAARNAGRSNRTTW-QP 394
QY 335 LVLVHLL 342
DB 395 LLAMMLL 402

RESULT 12
Q9VMB2 PRELIMINARY; PRT; 315 AA.
ID Q9VMB2;
AC Q9VMB2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CG11320 PROTEIN.
GN CG11320.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelthum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003614; AAF52409.1; -;
 DR Flybase: FBgn0031837; CG11320.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG_1like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 315 AA; 35487 MW; 4CC4DEAA45DA12B8 CRC64;

Query Match 18.4%; Score 333; DB 5; Length 315;
 Best Local Similarity 31.9%; Pred. No. 4.7e-21;
 Matches 94; Conservative 54; Mismatches 125; Indels 22; Gaps 11;

QY 33 SGDAIFPKAMDNVTVRQGESATLRCTIDNRVT-RVAML--NRSTILYAGNDKWCLDPRV 89
 Db 19 AADPKFSGPINNSTYFVGRDALLTCVVDLVSEFKVAMLRVDTQTLSIQNHVITKNHRIS 78
 QY 90 LLSNTQTQYSIEIQNDVDYDEGPTCSVQTDNHPKTSRV-HLIQVSPKIV--EISSDIS 146
 Db 79 ISHTEHRIMQLKIRVDQESDRGMQINTD--PMKSQGYLDVVPPIVDYQTSQDV 136
 QY 147 INEGNNISLTCTATGRPEPTVWRHISPKAVGFVSED---EYLEIQG-----ITREQS 196
 Db 137 RSTGQNVTLTCSATGVPMPITWRREATPL-LISDDGDRFVSVEGQNTLMQVQRSHM 195
 QY 197 GDVECSASNDVAPVVRKRVTVNYPYISEAKGT-GVPVQKGTLQCEASAVPSAEFQW 255
 Db 196 GAYLCIASNGVPTVSKRVMLVVFAPTIWIRYDTIYVGLGQKLTLECITESQPASVNF 255
 QY 256 YKDKRLIEGK-KGVKVEN-REFLSKLIFNVSEHDYGNITCVASNKLGHTNASI 308
 Db 256 LRDSQLLQGGSYESVSDVHVRIVMRITLRPTTKRDFGEYICRAKNAMGQTDRII 310

RESULT 13
 P91670 PRELIMINARY; PRT; 528 AA.
 AC P91670;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE KLINGON.
 GN KLG OR KLINGON OR CG6669.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Butler S.J., Ray S., Hiromi Y.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U78177; AAB36950.1; -;
 DR Flybase: FBgn0017590; Klg.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG_1like; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 528 AA; 58565 MW; B6C707A0A24806BC CRC64;

Query Match 17.1%; Score 308.5; DB 5; Length 528;
 Best Local Similarity 28.8%; Pred. No. 1.4e-18;
 Matches 85; Conservative 54; Mismatches 127; Indels 29; Gaps 10;

QY 36 AIFPKAMDNVTVRQGESATLRCTIDNRVT-RVAML--NRSTILYAGNDKWCLDPRVLSNT 94
 Db 98 APFPLQRTHLPRRRRGHAGLPQGVENLGNFVLLMRGTVNLTAASIMVTRDERVRLIDG- 156
 QY 95 QTQYSIEIQNDVDYDEGPTCSVQTD-NHPKTSRVHLIQVSPKIVEISSDISINEGNNI 153
 Db 157 ---YNEISIDLEPDQADGYVQISDKINRDQVHTVEILVPPSVRAIPTSGQLQARKGPI 213
 QY 154 SLTCTATGRPEPTVWRHIS--PRAVGFVSEDEYLEIQGITREQSGDYECASNDVAPV 211
 Db 214 TLECKSGSNPVPISYWTKKSGANKSTARIGDPIITLEKLEKQAGVYQCTADNGVDPV 273
 QY 212 VRRVAVTVNYPYISEAKG--TGVPVQKGTLQCEASAVPSAEFQWKD-----DKR 261
 Db 274 TVDMRLDVLVPPDIQVEKSWIHSG--EGFEAKLVCIVFADPVATVSWYQNSPIQSTDRI 331
 QY 262 LIEGKGVKVENRFLSKLIFNVSEHDYGNITCVASNKLGHTNASIMFG-PGA 315
 Db 332 IMATR-----ANRMLT---IKHIQEDFGNYSVADNSLGRSKRYMELSGRPGA 378

RESULT 14
 Q9VCT4 PRELIMINARY; PRT; 545 AA.
 AC Q9VCT4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE KLG PROTEIN (ID10776P).
 GN KLG OR CG6669.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003741; AAF56071.1; -
DR EMBL: AY060363; AAL25402.1; -
DR FLYBase: FBgn0017590; klg.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; ig_3.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00408; IGC2; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 545 AA; 60087 MW; D5E81D9E5574E9DE CRC64;

Query Match 16.9%; Score 306; DB 5; Length 545;
Best Local Similarity 28.9%; Pred. No. 2.4e-18;
Matches 86; Conservative 55; Mismatches 125; Indels 32; Gaps 12;

QY 36 ATEPKAMD-NVTVRQ--GESATLRCTIDNRVTRV-AWLNKSTIIYAGNDKWCIDPRVLL 91
DB 98 ATLPRFLSRGHTYRAVVGDTLVLPQOVENLGNFVLLMRGTINVLTAASNIMVTRDERVLI 157
QY 92 SNTQTOYSIEIQNVYDEGPTCSVQTD-NHPRKSRVHLIYQVSPKIVEISSDISINEG 150
DB 158 DG---YNLEISIDLEPQDAGDYVQCISDKINRQDVHTVEILVPPSVRAIFPSGQLQARKG 213
QY 151 NNISLTCTATGRPEPTVTRHIS--PKAVGFVSEDEYLEIQGITRQSGDYECASANDVA 208
DB 214 GPITLECKSGSNPVSISYWTKKSGANKSTARIGDPILITLEKLERQQAQVYQCTADNGVG 273
QY 209 APVVRKRVKVTNVPPIYSEAKG---TGVPVGQKGTLCQCEASAVPSAEFQWYKD----- 258
DB 274 DPVTVMRLDLVLPDQVEKSMHSG--EGFEAKLVCIIVADPVATVSWYQNSFPIQST 331
QY 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNKLGHTNASIMLFG-PGA 315
DB 332 DRRIMATR-----ANRHLT---IRHIQDEDFGNYSCVADNSLGRSRKYMELSGRPGA 381

RESULT 15
Q96SC3 PRELIMINARY; PRT; 2673 AA.
AC Q96SC3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE FIBULIN-6 (FRAGMENT).
GN FIBL-6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RA Kostka G., Timpl R.;
RT "Partial sequence of fibulin-6 with a c-terminal region related to
RT domain II and III of the fibulin family.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ306906; CAC37630.1; -
FT NON_TER 1 1
SQ SEQUENCE 2673 AA; 291017 MW; BEAEC30B8340E272 CRC64;

Query Match 16.1%; Score 290.5; DB 4; Length 2673;
Best Local Similarity 29.8%; Pred. No. 5.3e-16;
Matches 87; Conservative 36; Mismatches 106; Indels 63; Gaps 10;

QY 46 TVRQGESATLRCTIDNRVTRVAVWLNKSTIIYAGNDKWCIDPRVLLSNTQTOYSIE---- 101
DB 1217 TVNENSOAILPCVADGIPTPAI-----NWKKN--VLLANLIGKRYTAEPYGE 1261
QY 102 --IQNVYDEGPTCSVQTDNHPRKSRVHLIYQVSPKIVEISSDISINEGNNISLTCTIA 159
DB 1262 LIENVYLEDSEGFYTCVANNAGEDTHTVSLTVHYVLPFTTELPGDVSINKGEQLRLSCKA 1321
QY 160 TGRPEPTVW---RHISPKAVGFVSEDEYLEIQGITRQSGDYECASANDVA----- 208
DB 1322 TGIPPLRLTWTFTNNIIPAHFDSVNGHSELVIERYSKEDSGTYCTAENSYGVKAIQFV 1381
QY 209 ----APVVRKRVKVTNVPPIYSEAKGTGVPVGQKGTLCQCEASAVPSAEFQWYKDDKRLIE 264
DB 1382 YVKEPVPFKG-----DYPHWIE-----PLGNAAILNCEVKGDPPTTIQW----- 1421
QY 265 GKKGVKVENRPFSLKLI-----IFNVSEHDYGNITCVASNKLGHTNASIML 310
DB 1422 NRKGVDEIRISHRIQRLGNGSLAIYGTVNE-DAGDYTCVATNEAGVERSMSTL 1472

Search completed: July 12, 2002, 00:45:04
Job time: 682 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 21:28:00 ; Search time 2986.73 Seconds

(without alignments)
7650.623 Million cell updates/sec

Title: US-09-700-397-2

Perfect score: 1693
Sequence: 1 gtccctcagcaaacacgtg.....aaaaaaaaaaaaaaaaaaaa 1693

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	658	38.9	865	10	BI666583	BI666583 603291469
2	645	38.1	1015	9	AL533026	AL533026 AL533026
3	635.2	37.5	1039	10	BE798585	BE798585 601581610
4	631.8	37.3	870	10	BI913885	BI913885 603183295
5	627.6	37.1	732	10	BI551784	BI551784 603197479
6	612.4	36.2	784	10	BI549918	BI549918 603194765
7	600.8	35.5	604	9	AW025115	AW025115 wu71h04.x
8	593.2	35.0	770	9	AW117456	AW117456 xdg2a06.x
9	549	32.4	661	10	BM009450	BM009450 603629962
10	544.8	32.2	580	10	BI548566	BI548566 603189502
11	540.2	31.9	633	10	BG706987	BG706987 602672194
12	531.4	31.4	545	10	BE263639	BE263639 601192064
13	528.4	31.2	754	10	BI598759	BI598759 603245538
14	525.4	31.0	768	9	AU080629	AU080629 AU080629
15	486	28.7	486	9	AI753140	AI753140 CR05G10.x
16	485.6	28.7	953	10	BM423716	BM423716 AGENCOURT
17	471.2	27.8	671	9	BB644996	BB644996 BB644996

18	467.2	27.6	479	9	AA843782	AA843782 a118d10.s
19	457.4	27.0	524	9	BE014142	BE014142 125737 MA
20	455	26.9	979	10	BG261691	BG261691 602373361
21	453	26.8	522	10	BI553032	BI553032 603193672
22	450	26.6	849	10	BI755360	BI755360 603024964
23	447.6	26.4	553	10	BE864555	BE864555 UI-M-BH1-
24	443.4	26.2	456	9	AI369684	AI369684 qy71g03.x
25	440	26.0	548	9	BE015245	BE015245 127482 MA
26	437.4	25.8	440	9	AI118423	AI118423 q053g09.x
27	427.8	25.3	655	10	BI548049	BI548049 603196558
28	424.4	25.1	426	9	AI332824	AI332824 qp96e10.x
29	419.2	24.8	663	9	BB640070	BB640070 BB640070
30	408.4	24.1	806	9	AU051132	AU051132 AU051132
31	404.2	23.9	557	10	BM256660	BM256660 520043 MA
32	396.8	23.4	533	10	BI341675	BI341675 369186 MA
33	391.2	23.1	688	9	BB646531	BB646531 BB646531
34	388.8	23.0	754	10	BI550038	BI550038 603192502
35	374.4	22.1	376	9	AI246488	AI246488 q113q12.x
36	371	21.9	705	10	BG704152	BG704152 602687364
37	370	21.9	389	9	AA450107	AA450107 zx42d09.s
38	349.6	20.6	425	10	H87092	H87092 ys74g04.r1
39	346	20.4	346	9	AI951451	AI951451 wx67b07.x
40	340.2	20.1	478	10	H05429	H05429 y180h09.r1
41	334.4	19.8	336	9	AI262562	AI262562 qk42f01.x
42	332	19.6	579	9	BB644523	BB644523 BB644523
43	325	19.2	329	10	F06205	F06205 HSC10F041 n
44	310.2	18.3	602	9	BB611718	BB611718 BB611718
45	295	17.4	764	10	BI752729	BI752729 603028343

ALIGNMENTS

RESULT 1
BI666583
LOCUS
DEFINITION
603291469F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5310833 5',
mRNA sequence.
BI666583
ACCESSION
BI666583.1 GI:15580816
VERSION
EST.
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 865)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM11787 row: j column: 18
High quality sequence stop: 742.
Location/Qualifiers
1. 865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5310833"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-df primed using primer 5'-TTTCTTTTCTTTTCTTTT-3',
size-selected for average insert size 2.3 kb and

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 250 a 230 c 209 g 176 t

ORIGIN

Query Match 38.9%; Score 658; DB 10; Length 865;
Best Local Similarity 99.7%; Pred. No. 1.2e-84;
Matches 680; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 gtccttcagcaaaacagtgatttaaatctcttcgcaaacgttgagagacacatct 60
Db 55 GTCTTCAGCAAAACAGTGGATTAAATCTCTTCACACAGCTTGAGAGACACATCT 114

QY 61 atcaggaagaaagaaagaaagaaacagacctgacaaagaaagaaagaaagaa 120
Db 115 ATCAGGAAAGAAAGAAAG-AAAAAAACCGAAGCTGACAAAGAAAGAAAGAGAGA 173

QY 121 aaaaaatcatgataaacatccagccaaatgacaaatctctcttggcaatctc 180
Db 174 AAAAAAATCATGAAACCATCCAGCCAAAATGACAAATCTATCTCTGGCAATCTTC 233

QY 181 acggggtgctgtctgtctctcttcacagagtgccctgagcagcagagatgcc 240
Db 234 ACGGGGCTGGCTGCTCTGTCTCTTCCAGAGAGTGCCCGTGGCAGGAGATGCCACC 293

QY 241 ttccecaagctatgacaaagtgacgtgacggcagggagggagcagccctcaggtc 300
Db 294 TTCCCAAGGCTATGGACAAAGTGACGGTCCGGGAGGGGAGAGCCACCTCAGGTGC 353

QY 301 actattgacaacgggtcaccgggtggtggtggtggtggtggtggtggtggtggt 360
Db 354 ACTATTGACAAACGGGTGACCGGGTGGCTGGCTAAACCGCAGACCATCTCTATGCT 413

QY 361 gggaatgacaagtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 420
Db 414 GGGAAATGACAAAGTGGTGGCTGGATCCCTGGTGGTGGTGGTGGTGGTGGTGGTGG 473

QY 421 tacagcatcgagatccagaaagtgatggtatgacagagggcccttacacgtgctgtg 480
Db 474 TACAGCATCGAGATCCAGACGTGATGATGACGAGGGCCCTTACACCTGCTGGGTG 533

QY 481 cagacagacaacaccccaagacctctgaggtggtggtggtggtggtggtggtggt 540
Db 534 CAGACAGACAACCCCAAGACCTCTAGGGTCCACCTCATTTGCAAGTATCTCCAAA 593

QY 541 attgtagagatttcttcagatatctccatlaatgaagggaaac-aatatagcctcag 599
Db 594 ATTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGAAACAAATATTAGCCCAACCTG 653

QY 600 catagcaactggttagaccagagcctcaggttacttgagacacatctctcc-aaagcgt 659
Db 654 CATAGCAACTGCTAGACAGAGCCCTAGGTTACTTGAGACACACATCTCTCCCAAGCGGT 713

QY 660 tggcttgtgagtgagagcga 681
Db 714 TGGCTTGTGAGTGAAGACGAA 735

RESULT 2

AL533026 1015 bp mRNA linear EST 13-FEB-2001

LOCUS AL533026 LTI_FL015_Brn1 Homo sapiens cDNA clone CSODN005YD20 5

DEFINITION prime, mRNA sequence.

ACCESSION AL533026

VERSION AL533026.1 GI:12796519

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1015)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..1015

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODN005YD20"

/clone_1lb="LTI_FL015_Brn1"

/sex="male"

/tissue_type="Adult brain"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies.

Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT 295 a 249 c 251 g 219 t 1 others

ORIGIN

Query Match 38.1%; Score 645; DB 9; Length 1015;
Best Local Similarity 86.8%; Pred. No. 8e-83;
Matches 806; Conservative 1; Mismatches 1; Indels 121; Gaps 4;

QY 527 aagtatctccaaatgtagagatttctcagatatctccatlaatgaaggaacata 586
Db 90 AAGTATCTCCAAATTTAGAGATTCTTCAGATATCTCCATTATGAAGGACAATA 149

QY 587 ttagcctcaactcagtagcaactgtagaccagagcctcaggttacttgagacacatct 646
Db 150 TTAGCCTCACTGCATAGCAACTGTTAGACAGAGCCTACGGTTACTTGAGACACATCT 209

QY 647 ctcccaagcgggttggttctgtgagtggaagcgaatacttggaattcagggcaccacc 706
Db 210 CTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAAATTAATTGAGGGATCACCC 269

QY 707 gggaagcagtcagggagtagcagtggtggtggtggtggtggtggtggtggtggtggt 766
Db 270 GGGAGCAGTCAAGGGAGTACGAGTGCAGTGCCTCCAAATGACGCTGGCCGCGGTGATAC 329

QY 767 ggagagtaaaaggtcacccgtgaactatccaccatacttcagaagccaaggtacagtg 826
Db 330 GGAGAGTAAAGGTACCCGTGAACCTATCCACCATATTTCAGAAAGCCAAAGGTTACAGGTG 389

QY 827 tccccgtggacaagggagacactgagtggtgagcctcagcaggtccctcagcagaat 886
Db 390 TCCCGCTGGACAAAAGGGGACACTGCTAGTGAAGCCTCAGCAGTCCCTCAGCAGAT 449

QY 887 tccagtgtagaaggtgacaaa----- 910
Db 450 TCCAGTGTGTACAAAGATGACAAAGAGCTGAATCTCATTCACAGTTGGTTATGATGGG 509

QY 911 ----- 910

Db 510 AAAGCTTCCTCCCATGGTGGACGAATGGTGTCAAAAGGCCAGTGGGATCAATCAGCCT 569

QY 911 -----gactgattgaagaaagaaaggggtgaaagtgaagaaac 948

Db 570 GACTTGCTCGAGAAATCTCCCGACTGATTGAAGGAAGAGGGGTGAAGGTGAAAAAC 629

QY 949 agaccttctctcaaaactcctctcctcaatgtctctgacatgactatgggaactac 1008
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Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	630	AGACCTTTCTCTCAAAACCTCATCTTCTTCATGATGTCTCTGAACATGACTATGGGAACATAC						
QY	1009	acttgccgtgacctccacaacagctggygccacaaccaatgcccagcatcatgtatttggtcca						
Db	690	ACTTGCGTGGCCTCCAAACAAGCTGGGCGACACCAATGGCAGCATCATGCTATTGGTCCA						
QY	1069	ggcgccgtcagcgaggtgagcaacgycacagctcgagggagggcaggtcggtctgctgctg						
Db	750	GGCGCCGTCAAGCGAGGTGAGCAACGGCAGTCGAGGAGGGCAGGCTGGCTGGCTG						
QY	1129	cctctctgtgcttgacacctgcttctctaaatttgatgtgagtgccacctccccaccg						
Db	810	CCTCTTCTGTCTCTTGACCTGCTTCTCAATTTTGATGTGAGT-SCACTTCCCGACCCGG						
QY	1189	gaaagctgcccgcaccaccaccaccacaacacagcaatgycacaacgcagacaacca						
Db	869	GAAAGGCTGCCGCCACCAACCACCAACACACAACAGC-ATGGCAACACCGACAGCAACCA						
QY	1249	atcagatatatacaaatgaaattagagaagaacacagcctcatggyacagaatttgaggy						
Db	928	ATCAGATATATACAAATGAATTTAGAGAACAACACAGCCTCATGGGACAGAATTTGAGGG						
QY	1309	aggggacaacaagaatacttgygggggaaa						
Db	988	AGGGG-ACAAAGAAATACTTTGGGGGAAAA						
RESULT	3							
LOCUS	BE798585	1039 bp	MRNA	linear	EST	20-SEP-2000		
DEFINITION	601581610F1 NTH_MGC_7	Homo sapiens	CDNA	clone	IMAGE:3935955	5'		
VERSION	BE798585							
KEYWORDS	BE798585.1	GI:10219783						
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
TITLE	1 (bases 1 to 1039)							
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgapbs-r@mail.nih.gov							
	Tissue Procurement: DCTD/DRP							
	CDNA Library Preparation: Ling Hong/Rubin Laboratory							
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov							
	Plate: L1CM779 row: d column: 04							
	High quality sequence stop: 849.							
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Source	1. 1039							
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	/db_xref="taxon:9606"							
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	/clone_lib="NIH_MGC_7"							
	/tissue_type="small cell carcinoma"							
	/cell_line="MGC3"							
	/lab_host="DH10B (phage-resistant)"							
	/note="Organ: lung; Vector: pCMB7; Site_1: XhoI; Site_2:							
	EcoRI; CDNA made by oligo-dT priming. Directionally							
	cloned into EcoRI/XhoI sites using the following 5'							
	adaptor: GGCACGAG(G). Size-selected >500bp for average							
	insert size 1.8kb. Library constructed by Ling Hong in							
	the laboratory of Gerald M. Rubin (University of							
	California, Berkeley) using ZAP-cDNA synthesis kit							
	(Stratagene) and Superscript II RT (Life Technologies)."							
BASE COUNT	274 a 271 c 286 g 207 t							
ORIGIN	1 others							

Query Match	37.5%;	Score 635.2;	DB 10;	Length 1039;
Best Local Similarity	97.6%;	Pred. No. 2e-81;		
Matches 656;	Conservative 0;	Mismatches 13;	Indels 3;	Gaps 1
QY 294	caagltgcactattgacaacccgggtcaccccggtggtgcctgtgcttaaacgcgcacatcct	353		
Db 65	CAAGTGCACCTATGTGACAACCCGGGTGCGCCCGGGTGGCCCTGGCTAAACCGCACACCATCCT	124		
QY 354	ctatgctgggaatgacaaggtgtgccttgatctcctgcgtgtgtccttcttgagcaacacca	413		
Db 125	CTATGCTGGGAATGACACAAGTGTGCCCTGATTCCTCGCGTGGTCTTCTTGAGCACACACCCA	184		
QY 414	aacgcagttacagcatcgagatccagaacgttggatgtgtatgacgagggcccttacactg	473		
Db 185	AACGCAGTACAGCATCGAGATCCAGAACGTTGATGTATGACGAGGGCCCTTACACCTG	244		
QY 474	ctcgtgtcaacagacaacaccccaagaacctctagggtccacactatgttgaagtatc	533		
Db 245	CTCGGTGCAGACGACACACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATC	304		
QY 534	tcccaaaattgttagagattcttccagatctccatataatgaaggaacataattagct	593		
Db 305	TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCT	364		
QY 594	caactgcataagcaactgtgtagaaccagagccttaacggttactttgagacacatcttccaa	653		
Db 365	CACCTGCATAGCAACTGTGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCAA	424		
QY 654	agcgtgtgtcttgttgaagtgaaagcaatacttgaattccagggtcatcaccccgagca	713		
Db 425	AGCGGTGTGCTTTGTGATGGAAGACGAATACTTGAATTCAGGGCATTCACCCGGGAGCA	484		
QY 714	gtcaggggactacagagtgagtgccctcccaatgacgtgtgcccgcgctgtgtacgagagt	773		
Db 485	GTCAGGGGACTACGAGTGCAGTGCCTCCCAATGACGTGGCCCGCCCGGTGTACGAGAGT	544		
QY 774	aaaggtcacccgtgaactatccaccataaatttcagaagccaagggtacaggtgtcccggt	833		
Db 545	AAAGGTCAACCGTGAACCTTCCACCATATTTTCAGAAAGCCAAAGGTACAGGTGTCCCGGT	604		
QY 834	gggacaaaaggggacactgacgtgtgaagcctcagcagctccctcagcagaattccagtg	893		
Db 605	GGGACAAAAGGGACACTGCAGTGTGAAGCCCTCAGCAGATCCCTCAGCAGAAATTCAGATG	664		
QY 894	gtacaagatgacaanaagactgatgaagaa--agaagaagggtgaaggtgaaacag	950		
Db 665	GTACAAGGATGACAAAAGACTGATTGGAAGGAACAGACAGGGGTGAACAGTTGAAACACAG	724		
QY 951	accttcctctc 962			
Db 725	ACCTTTTTCCTC 736			
RESULT 4				
LOCUS B1913885	870 bp	mRNA	linear	EST 16-OCT-2001
DEFINITION 603183295F1 NIH_MGC_121	Homo sapiens	CDNA	clone IMAGE:5247550	5',
ACCESSION B1913885				
VERSION B1913885				
KEYWORDS B1913885.1	GI:16178206			
SOURCE EST.	human.			
ORGANISM Homo sapiens				
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE NIH-MGC http://mgi.nci.nih.gov/.				
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgaabs-r@mail.nih.gov				
Tissue Procurement: Life Technologies, Inc.				

QY 241 ttccccaagtctatgacacgtgacgtccgagggagagagcgccaccctcaagttgc 300
|||||
Db 299 TTCCCCAAGCTATGGACAACCTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGC 358
QY 301 actattgacaaccgggtcaccgggtgtgctgtgctaaccgagcaccatctctatgct 360
|||||
Db 359 ACTATGTACAACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCT 418
QY 361 gggaatgacaagtgtgtgctgtgatacctgcgtgtgtctctgtgacaacccaagcgag 420
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Db 419 GGGATGACAGATGGTGGCTGGATCCCTCGCTGTCTCTGTGAGCAACACCAAGCGCAG 478
QY 421 tacagcatcgagatccagaacgtgtgtgtatgacgagggcccttaacctgtgtgtg 480
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Db 479 TACAGCATCGAGATCCAGAACGTGATGTATGACGAGGGCCCTTACACCTGCTGCGTG 538
QY 481 cagacagacaaccaccaagaacctctaggggtccacctcatlgtgcaagtatctccaaa 540
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Db 539 CAGACAGACANCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAA 598
QY 541 attgtagagatttcttcagatatctccattaatgaagggaacaatatagacctcctgc 600
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Db 599 ATTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGGAACAATATTAGCCTCAGCTGC 658
QY 601 atagcaactgtgtagaccagagcctactgttactgtg-agaacatctctcccaagcggt 659
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Db 659 ATAGCAACTGTGTAGACCGACGCTACGGTTACTTGAAGACACATCTCTCCCAAGCGG- 717
QY 660 tggcttctgtgagtgta 674
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Db 718 TGGCTTTGTGAGTGA 732

RESULT 6
B1549918 784 bp mRNA linear EST 05-SEP-2001
LOCUS B1549918 603194765F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274161 5',
DEFINITION mRNA sequence.
ACCESSION B1549918
VERSION B1549918
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palakovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1692 row: b column: 18
High quality sequence stop: 726.
location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
human."

size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 234 a 211 c 184 g 155 t
ORIGIN

Query Match 36.2%; Score 612.4; DB 10; Length 784;
Best Local Similarity 98.2%; Pred. No. 3.8e-78;
Matches 662; Conservative 0; Mismatches 6; Indels 6; Gaps 4;

QY 1 gtccttcagcaaaaacagtgatttaaatctccttgcaagaagcttgagagcaacaatct 60
|||||
Db 65 GTCTTACGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGACCAACAATCT 124
QY 61 atcaggaagaagaagaagaaaaaacgaacctgacaagaaagaagaagaaga 120
|||||
Db 125 ATCAGGAAGAAAGAAAG-AAAAAACCGAACCTGACAAAAAGAGAGAGAGAGA 183
QY 121 aaaaaatcatgaaacatccagccaaanaatgcacaattctatctcttggcaatctc 180
|||||
Db 184 AAAAAATCATGAAACCATCCAGCCAAAATGCACAATTCTATCTCTTGGCAATCTTC 243
QY 181 acgggctgtgtctgtgtctcttccaaagagtgccgctgagcagcgagatgccacc 240
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Db 244 ACGGGCTGGCTGCTGTGTCTCTTCCAAAGAGTCCCGTCCGACGGAGATGCCACC 303
QY 241 ttccccaagtctatgacaacgtgacgtccgagggagagcgccaccctcaagttgc 300
|||||
Db 304 TTCCCCAAGCTATGAGACAACGTGACGGTCCGGCAGGGGAGAGAGCCACCTCAGGTGC 363
QY 301 actattgacaaccgggtcaccgggtgtgctgtgctaaccgagcaccatctctatgct 360
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Db 364 ACTATGTACAACCGGGTCAACCGGGTGGCTGCTGCTAAACCGCAGCACCATCTATGCT 423
QY 361 gggaatgacaagtgtgtgctgtgatacctgcgtgtgtctctctgtgacaacccaagcgag 420
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Db 424 GGAATGACAAGTGTGCTGTGATCTCGCTGCTGCTCTGTGACCAACCAACCGCAG 483
QY 421 tacagcatcgagatccagaacgtgtgtgtatgacgagggcccttacacctgtcgtgtg 480
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Db 484 TACAGCATCGAGATCCAGAACGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTG 543
QY 481 cagacagacaaccaccaagaacctctaggtgtccacctcatlgtgcaaglatctccaaa 540
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Db 544 CAGACAGACAACCCCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAA 603
QY 541 attgtagagatttcttcagatatctccattaatgaagggaacaatatagacctca-ccgtg 599
|||||
Db 604 A-TGTAGAGATTCTTCAGATATCTCCATTATGAAGGAACAATATTAGCCTCACCTG 662
QY 600 catagcaactgtgtagaccagagcctactggttactgtgagacac--atctctcccaagc 656
|||||
Db 663 CATAGCAACTGTGTAGACCAAGACCTACGGTTACTTGGAGACACCATCTCCCCCAAAAGC 722
QY 657 ggttggcttgtgta 670
|||||
Db 723 GGTGGCTTCGCGA 736

RESULT 7
AW025115/c 604 bp mRNA linear EST 09-MAR-2000
LOCUS AW025115
DEFINITION wu71h04.x1 NCI_CGAP Kid3 Homo sapiens cDNA clone IMAGE:252527 3',
similar to SW:NTRI_RAT Q62718 NEUROTRIMIN PRECURSOR ;, mRNA
sequence.
ACCESSION AW025115
VERSION AW025115
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 604)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/lml.lnl.gov
Insert Length: 1662 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
1. 604
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2525527"
/clone_lib="NCI-CGAP_Kid3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 118 a 158 c 157 g 171 t
ORIGIN

Query Match 35.5%; Score 600.8; DB 9; Length 604;
Best Local Similarity 99.7%; Pred. No. 1.8e-76;
Matches 602; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1063 ggtccagggcgccgtcagcgaggtgagcaacgacgtcgagggcgagcggtcgtctgg 1122
    |||||||
Db 604 GGTCCAGGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCGGCTGCGTGG 545

QY 1123 ctgtctcctcttctgtctgtcgaacctgtctcaatttgatgtgagtgccactccc 1182
    |||||||
Db 544 CTGCTGCTCTTCTGTGCTTGCATGCTCTCTCAAAATTTGATGTGAGTGCACCTTCCC 485

QY 1183 acccgggaaagctgcgcgccaccaccacacacacagcaatgcaacaccgacag 1242
    |||||||
Db 484 ACCCGGAAAGGCTGCCGCCACCACACACACACACCAATGCAACACCGACAG 425

QY 1243 caaccaatcagatatatacaaatgaatagaagaacacagcctcatgggacagaatt 1302
    |||||||
Db 424 CAACCAATCAGATATATACAAATGAAATAGAAAGAACACAGCCTCATGGGACAGAAATT 365

QY 1303 tgaaggaggggaacaagaatacttgggggggaaaaagttttaaaaaagaattgaaa 1362
    |||||||
Db 364 TGAGGGAGGGGAACAAGAACTTTGGGGGGAAGAGCTTTTAAAAAAGAAATTTGAAAA 305

QY 1363 ttgccttcagatatattagttacaatggagtttcttctcccaaacggggaagaacagc 1422
    |||||||
Db 304 TTGCCTTCAGATATTATTAGTACAAATGGAGTTTCTTTTCCAAACGGGGAAGACACAGC 245

QY 1423 aaaccggcttgagcccaactgcaagctgcacgtgcgaacctcttggtgccaagtgggc 1482
    |||||||
Db 244 AACACCGGCTTGAGACCCACTGCAGAGCTGCATCGTGAACCTCTTTGGTGCACAGTGGGC 185
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QY 1483 aaggctcagctctcttgcgccacagagtgcgccccacgttgtaaacattctgagctggccat 1542
    |||||||
Db 184 AAGGCTCAGCCTCTCTGCCACAGAGTGCCTCCACAGTGAACATTCTGAGCTGGCCAT 125

QY 1543 cccaaattcaatcagttccatagagacgaagaatgagacctccggcccaagctggcg 1602
    |||||||
Db 124 CCCAAATTCATCAGTCCATAGAGACGAACGAATGAGACCTTCCGGCCCAAGCGTGGCG 65

QY 1603 ctgcggcacttggtgtagctgtgccaccacggcggtgtgtgtgtaaacgtgaataaaaa 1662
    |||||||
Db 64 CTGCGGGCAGCTTTGGTAGACGTGTGCCACACAGCGCGTGTGTGTGAACGTGAATAAAAA 5

QY 1663 gagg 1666
    |||
Db 4 GAGC 1
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RESULT 8
AW117456/c 770 bp mRNA linear EST 20-OCT-1999
LOCUS
DEFINITION
xd92a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2605042 3' similar to SW:NTRI_RAT Q62718 NEUROTRIMIN
PRECURSOR ; , mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW117456
AW117456.1 GI:6086040
EST.
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
1. 770
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2605042"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"

FEATURES
source

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 155 a 190 c 195 g 230 t
ORIGIN

Query Match 35.0%; Score 593.2; DB 9; Length 770;
Best Local Similarity 97.8%; Pred. No. 2.1e-75;
Matches 612; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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QY 1045 gccagcatcgtatattggtccagggcgccgtcagcgaggtgagcaacggcagctgaggg 1104
    |||
Db 625 GCCCTGACCTTTGAAAAGGTCAGGGCGGCTCAGCGAGGTGAGCAACGGCACGTCGAGG 566

QY 1105 agggcagctgcgtctgtgctcttctgtgttgcacctgcttcaaattttga 1164
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Db 565 AGGGCAGGCTGCCTGTGGCTGCTGCCCTCTTCTGGTCTTGCAACCTGCTTCTCAATTTTGA 506
 QY 1165 tgtgagtgcacacttccccaccccggaagygctgcgcgccaccaccaccaccacaacag 1224
 Db 505 TGTGAGTGCCTACTTCCCCACCCGGGAAGGCTGCCGCCA-CACCACCACCACACAACAG 447
 QY 1225 caatgccaacacccgcagcaaccaatcagatatatacaaaatgaattgaagaacaacag 1284
 Db 446 CAATGGCAACACCGGACAGCAACCAATCAGATATATACAAATGAATTTGAAGAAACACAG 387
 QY 1285 cctcatggagacagaatttgaaggagggaacaagaataactttggygggaaaaaagttt 1344
 Db 386 CCTCATGGAGACAGAAATTTGAGGAGGGGAACAAGAATACTTTGGGGGGAAGAAGTTT 327
 QY 1345 taaaaaagaanaattgaanaattgccttgcagatatattagytacaatgagtttcttltccc 1404
 Db 326 TAAAAAAGAATTTGAATAATTGCCCTTGCAATATTAGGTACAATGGAGTTT TTTTCCC 267
 QY 1405 aaacgcygaagaacacacagcacaccccgcttgyaaccactgcaagctgcatcgtgcaacctc 1464
 Db 266 AAACGGGAAGAACACACACACACACCCCGCTTGGACCCCACTGCAAGCTGCATCGTCAACCTC 207
 QY 1465 ttgtgtccagttgtggycaagggctcagcctctctgcccacagagtgcgcccaagttgaa 1524
 Db 206 TTTGTGTCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCCACAGAGTGTCCTCCACGTTGAA 147
 QY 1525 catctcgtgagctggtccatcccaattcaatcagtcacatagagacgaacagaatgagact 1584
 Db 146 CATCTGTGAGAGCTGGCCCATCCCAAAATTCATCAGTCCATAGAGACGACAGATGAGACT 87
 QY 1585 tccgcccccaagcgtggtgcgtgcyggtgcaacttgytagactgtgcccaccagcgtgtgttg 1644
 Db 86 TCCGGCCCAAGCGTGGCCCTGCGGGCACTTTGGTGAAGTGTGCCACACGCGGTGTGTG 27
 QY 1645 tgaacgctgaataaaaaagaagcaaaa 1670
 Db 26 TGAACGTTGAATATAAAGAGCAAGA 1

RESULT	9
LOCUS	BM009450
DEFINITION	661 bp mRNA linear EST 30-OCT-2001
ACCESSION	603629962F1 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5443743 5',
VERSION	BM009450
KEYWORDS	mRNA sequence.
SOURCE	BM009450.1 GI:16523804
ORGANISM	EST. human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 661)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L1CML1921 row: 1 column: 16 high quality sequence stop: 659.

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FEATURES
  source
    Location/Qualifiers
      1. .661
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:5443743"
         /clone_lib="N1H_MGC_41"
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/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

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Query Match	32.48;	Score 549;	DB 10;	Length 661;
Best Local Similarity	94.68;	Pred. No. 4.2e-69;		
Matches 625;	Conservative	0;	Mismatches 0;	Indels 36;
				Gaps 4;
QY 657	ggttgcttltgtagtgaaagacgaatacttgaataatcaggycatcacccggagcagtc	716		
Db 1	GGTTGGCTTTGTGAGTGAAGACGAATACTTGAATAATTCAGGGCATCACCCGGAGCAGTC	60		
QY 717	aggagactacgagtcgagtcgctccaatgacgtgcccgcgcccgtgtacgagagtaaa	776		
Db 61	AGGGACTACGAGTGCAGTCGCTCCCAATGACGTGGCCGCCCGTGTACGGAGAGTAAA	120		
QY 777	ggtcacctgaactatccaccatacatctcagaagccaaggtacaggtgtcccccgtgg	836		
Db 121	GGTCAACCGTGAACATATCCACCATAATTTCAGAAGCCAAGGTACAGGTGTCCCCCGTGGG	180		
QY 837	acaaaaggggacacitgcagttgtgaagccctcagcagtcctccctcagcagaattccagtygta	896		
Db 181	ACAAAAGGGGACACITGCAGTGTGAAGCCCTCAGCAGTCCCCCTCAGCAGAATTCAGTGTGTA	240		
QY 897	caaggatgacaaaagactgattgaaagaaaggggtgtgaaatggaataacagaccctt	956		
Db 241	CAAGGATGACAAAAGACTGATTTGAAGAAAGAGGGGTGAAGATGGAAACACAGACCTTT	300		
QY 957	ccctccaaaactcatcttcttcaatgtctctgaacatgactatggyaactacacttgcgt	1016		
Db 301	CCCTCCAAAACCTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCT	360		
QY 1017	ggcctccacaacagcttggccacacaaatgccaagcatcatgtcattt-----	1062		
Db 361	GGCCTCCACAACAGCTGGGCCACACCATAATGCCAGCATCATGTCTATTGAGTGAAACTAC	420		
QY 1063	-----ggtccaggcgccgtcagcgcgaggtgacaaacygcagtcgag	1103		
Db 421	AGCCCTGACCCCTTTGGAAGGTTCCAGGCGCCGTCAGCGAGGTGACCAACGGCACGTCGAG	480		
QY 1104	gagggcaggcgtgcgtctgtgctgtgcctctctctgtgtctltgcaactgtctcnaatttg	1163		
Db 481	GAGGGCAGGCTGCGCTGTGGCTGTGCTCTCTTGTGGTCTTGTGCACCTGCTTCTCAATTTTG	540		
QY 1164	atgtgagtcgccacttccccaccgcgggaaagcgtgcgcgcaaccaacc-accacaacacaac	1222		
Db 541	ATGTGAGTGCACCTTCCCAACCCGGGAAAGGCTGCGCCGACCAACCGAACCAACAAC	600		
QY 1223	ag-caatgcaacaaccgacagaacc-aatcagatatatacaaatgnaattagaagaaac	1280		
Db 601	AGCCAATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAGAAAC	660		
QY 1281	a 1281			
Db 661	A 661			

RESULT	10
BI548566	
LOCUS	
DEFINITION	BI548566 580 bp mRNA linear EST 05-SEP-2001
ACCESSION	603189502F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5260753 5', mRNA sequence.
	BI548566

VERSION	BI548566.1	GI:15435878
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 580)	
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

Plate: LLAM11657 row: d column: 02
 High quality sequence stop: 580.
 Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .580

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5260753"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to ROP 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

```

Query Match	32.28;	Score 544.8;	DB 10;	Length 580;
Best Local Similarity	99.38;	Pred. No. 1.7e-68;		
Matches 568; Conservative	0;	Mismatches 2;	Indels 2;	Gaps 2;

QY 80 aaaaaaacccgaacctgacaaaaaagaanaaaagaagaagaaaaaataatcatgaaaccca 139
 |||||||
 Db 10 AAAAAAACCGAACCTGCACAAAAAGAGAAAGAGAGAAAAAATCATGAACAACCA 69
 QY 140 tccagccaaaatgacaaatctatctctgggcaatcttcacgyggtgctgtgt 199
 |||||||
 Db 70 TCCAGCCAAAAATGCACCAATCTATCTCTGGGCAATCTTCAGGGGCTGGCTGCTCTGT 129
 QY 200 gtctcttccaagagtgcccggtgcgcagcggagatgccaacttcccaaaagtatygac- 258
 |||||||
 Db 130 GTCTCTTCCAAGAGAGTGCCTCCGTGCAGCGGAGATGCCACTTCCCAAGCTATGGACA 189
 QY 259 aacgtgacggtccgycgaggggagagcgcacccctcaggtgcactattgacaacccggtc 318
 |||||||
 Db 190 AACGTGACGGTCCCGGCGAGGGGAGAGCGCCACCCCTCAGGTGCACATGGACAACCGGGTC 249
 QY 319 acccggtgycctggtctaaccgcgacgacocatctctatgtctyggaaatgacaagtgtgtc 378
 |||||||
 Db 250 ACCCGGGTGGCCCTGGGCTAAACCGCAGCACCATTCTCTATGCTGGGAATGACAAGTGTGTC 309
 QY 379 ctggtatcctcgcggtgtgtcctctctgagcaacaaccaaacgcagttacagcatcggaatccag 438
 |||||||
 Db 310 CTGGATCTCTCGCGGTGTCCTTCTGAGCAACACCCCAACGCAGTACAGCATCGAATCCAG 369
 QY 439 aacgtgagtgtgtatgaagagggcccttaacacctgtcgtgcgtgacagacaacaccca 498
 |||||||

Db	370	AACTGGATGTGTATGACGAGGGCCCTTACACCTGCTGGGTGCAGACAGACAACCA	429
QY	499	aagacctctagggtccacctcaattgtgcaagtatctccaaatgttagaattctca	558
Db	430	AAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCCCCAAAA-TGTAGAGATTCTTCA	488
QY	559	gatatctcattaatgaaggyaacaatattagcctcaactgcatagcaactgttagacca	618
Db	489	GATATCTCATTATGAGGGAMCAATATTAGCCTCACTGCATAGCAACTGTAGACCA	548
QY	619	gagcctacggttacttgtagagacacatctctcc	650
Db	549	GAGCCTACGGTTACTTGGAGACACATCTCTCC	580

RESULT	11				
LOCUS	BG706987	633 bp	mRNA	linear	EST 07-MAY-2001
DEFINITION	602672194F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4794790 5', mRNA sequence.				
ACCESSION	BG706987				
VERSION	BG706987.1	GI:13982882			
KEYWORDS	EST.				
SOURCE	human.				

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 633)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10676 row: 1 column: 23
High quality sequence stop: 633.

FEATURES	Location/Qualifiers
source	1. .633

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/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3'
and size-selected for average insert size 2.3 kb and
normalized to RQF 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

```

[illegible]

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|||||
Db 115 ATCAGGAAGAAAGAAAG-AAAAAAAAACCGAAGCTGACAAAAAGAGAAAAAGAGAGA 173
QY 121 aaaaaaatcatgaaaccatccagccaaatgacaaattctatctctggcaatctc 180
Db 174 AAAAAATCATGAAACCATCCAGCCAAAAATGCACAATCTATCTCTGGCAATCTTC 233
QY 181 acggggtgctgctctgtgtctctcctcgaaggagtgcccggtgcgcagggagatgccacc 240
Db 234 ACGGGGCTGGCTGCTGTGTCTCTTCCAGGAGTGCCCGTGGCGAGGGAGATGCCACC 293
QY 241 tcccccaagctatgacaaagtgaacgtgacggtccggcagggggagagagccaccctcaggtgc 300
Db 294 TTCCCCCAAGCTATGACACAGGTGACGGTCCGGCAGGGGAGAGGCCCACTCAGGTGC 353
QY 301 actattgacaaacgggtcaccgggtggtgcctggttaaacggcagcaaccatcctatgct 360
Db 354 ACTATTGACACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCT 413
QY 361 ggggaatgacaaagtgtgtcctggtatcctgcgtgtgtcctctgagcaacacccaaacgag 420
Db 414 GGGAAATGACAAAGTGTGCTGCTGATCTCTGCTGCTGAGCAACA-CCAAACGCGAG 472
QY 421 tacagcatcgagatccagaacgtgtgatgtatgacaggggacctacacctgtcgtgtg 480
Db 473 TACAGCATCGAGATCCAGAACGTGATGTATGACGAGGGGCCCTTACACCTGCTGAGTG 532
QY 481 cagacagacacacccaaagacctctaggtgccacctatgtgcaagtatctccaaa 540
Db 533 CAGACAGACAAACACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAA 592
QY 541 at-tgtagagattcttcagatatctcattaatgaaggga 580
Db 593 ATAGGTAGAGATTCTTCAGATATCTCCATTAATGAAGGGA 633

RESULT 12
BE263639 545 bp mRNA linear EST I3-JUL-2000
LOCUS 601192064F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536127 5',
DEFINITION mRNA sequence.
ACCESSION BE263639
VERSION BE263639.1 GI:9137183
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 545)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Plate: LCM217 row: p column: 16
High quality sequence stop: 545.
Location/Qualifiers
1. 545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3536127"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
BASE COUNT 162 a 134 c 144 g 105 t
ORIGIN
Query Match 31.4%; Score 531.4; DB 10; Length 545;
Best Local Similarity 99.6%; Pred. No. 1.4e-66;
Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 400 ctgagcaacaccccaaacgcaggtacagcatcgagatccagaacggtgatatgacgag 459
Db 1 CTGAGCAACACCCCAACCCAGTACAGCATCGAGATCCAGAACCTGTGATGACGAG 60
QY 460 ggccttacacctgctcgtgtgacagacaaaccacaaagaacctcaggtccacctc 519
Db 61 GGCCCTTACACCTGCTCGGTGACAGACAGCAACCAACCAAGACCTTAGGGTCCACCTC 120
QY 520 attgtgcaagtatctccaaatgttagagattctcagatatctccattaatgaagg 579
Db 121 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTCTTCAGATATCTCCATTATGAAGG 180
QY 580 aacaaatagcctcaccctgcatagcaactgttagaccagagcctacggttacttgaga 639
Db 181 AACAAATATTAGCTTCACTGCATAGCAACTGTAGACCAAGAGCCCTTACTTGAGA 240
QY 640 cacatctccccaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 699
Db 241 CACATCTCTCCCAAGCGGTTGGCTTGTGAGTGAAGACGAATCTTGAATTCAGGGC 300
QY 700 atcaccgggagcagtcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 759
Db 301 ATCACCAGGAGGAGCAGTCAAGGGGAGTACAGTGTGAGTGTGAGTGTGAGTGTGAGT 360
QY 760 gtgtgacggaagtaaggtacacgtgaactatccaccatcattcagaagccaaggt 819
Db 361 GTGTACGGAAGTAAGGTACCGGTGAACCTATCCACCATATTCAGAAAGCCAAAGGGT 420
QY 820 acaagtgcccccgtgtggaacaaagggagacatgagtgagtgagtgagtgagtgagtgag 879
Db 421 ACAGGTGTCCTCCGTTGGGCAAAAGGGGACACTGCAGTGTGAAGCCTTCAGCAGTCCCTCA 480
QY 880 gcaqaattccagtggtacaaagatgacaaagactgattgaagga-gaaaggggtgaa 938
Db 481 GCACAATTCCAGTGTGACAAAGATGACAAAGACTGATTGAAGGAACGAAGGGGTGAA 540
QY 939 agtgg 943
Db 541 AGTGG 545

RESULT 13
BI598759 754 bp mRNA linear EST 07-SEP-2001
LOCUS 603245538F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5287832 5',
DEFINITION mRNA sequence.
ACCESSION BI598759
VERSION BI598759.1 GI:15491698
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2002, 00:32:21 ; Search time 418.18 Seconds

(without alignments)
6816.544 Million cell updates/sec

Title: US-09-700-397-2

Perfect score: 1693
Sequence: 1 gtccttcagcaaacacagtgg.....aaaaaaaaaaaaaaaaaa 1693

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1156321 segs, 841861299 residues

Total number of hits satisfying chosen parameters: 2312642

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCIT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661.4	98.1	1679	5	US-09-978-403A-522 Sequence 522, App
2	1661.4	98.1	1679	5	US-09-978-544A-522 Sequence 522, App
3	1661.4	98.1	1679	5	US-09-978-681A-522 Sequence 522, App
4	1661.4	98.1	1679	5	US-09-978-757A-522 Sequence 522, App
5	1661.4	98.1	1679	5	US-09-978-564A-522 Sequence 522, App
6	1661.4	98.1	1679	5	US-09-999-831A-522 Sequence 522, App
7	1661.4	98.1	1679	5	US-09-999-829A-522 Sequence 522, App
8	1661.4	98.1	1679	5	US-09-978-375A-522 Sequence 522, App
9	1661.4	98.1	1679	5	US-09-978-423A-522 Sequence 522, App
10	1661.4	98.1	1679	6	US-10-013-921A-522 Sequence 522, App
11	1661.4	98.1	1679	6	US-10-013-929A-522 Sequence 522, App
12	1661.4	98.1	1679	6	US-10-013-918A-522 Sequence 522, App
13	1661.4	98.1	1679	6	US-10-017-082A-522 Sequence 522, App
14	1661.4	98.1	1679	6	US-10-119-480-125 Sequence 125, App
15	1661.4	98.1	1679	6	US-10-121-049-375 Sequence 375, App
16	1661.4	98.1	1679	6	US-10-121-050-375 Sequence 375, App
17	1661.4	98.1	1679	6	US-10-121-053-375 Sequence 375, App
18	1661.4	98.1	1679	6	US-10-121-043-375 Sequence 375, App
19	1661.4	98.1	1679	6	US-10-121-044-375 Sequence 375, App
20	1661.4	98.1	1679	6	US-10-121-047-375 Sequence 375, App
21	1661.4	98.1	1679	6	US-10-121-054-375 Sequence 375, App
22	1661.4	98.1	1679	6	US-10-121-056-375 Sequence 375, App
23	1661.4	98.1	1679	6	US-10-121-057-375 Sequence 375, App
24	1661.4	98.1	1679	6	US-10-121-058-375 Sequence 375, App
25	1661.4	98.1	1679	6	US-10-121-060-375 Sequence 375, App
26	1661.4	98.1	1679	6	US-10-121-063-375 Sequence 375, App

27	1661.4	98.1	1679	6	US-10-123-108-375 Sequence 375, App
28	1661.4	98.1	1679	6	US-10-123-154-375 Sequence 375, App
29	1661.4	98.1	1679	6	US-10-123-156-375 Sequence 375, App
30	1661.4	98.1	1679	6	US-10-123-157-375 Sequence 375, App
31	1661.4	98.1	1679	6	US-10-123-212-375 Sequence 375, App
32	1661.4	98.1	1679	6	US-10-123-213-375 Sequence 375, App
33	1661.4	98.1	1679	6	US-10-123-109-375 Sequence 375, App
34	1661.4	98.1	1679	6	US-10-121-041-375 Sequence 375, App
35	1661.4	98.1	1679	6	US-10-121-045-375 Sequence 375, App
36	1661.4	98.1	1679	6	US-10-121-046-375 Sequence 375, App
37	1661.4	98.1	1679	6	US-10-121-051-375 Sequence 375, App
38	1661.4	98.1	1679	6	US-10-121-048-375 Sequence 375, App
39	1661.4	98.1	1679	6	US-10-121-052-375 Sequence 375, App
40	1661.4	98.1	1679	6	US-10-121-061-375 Sequence 375, App
41	1661.4	98.1	1679	6	US-10-121-042-375 Sequence 375, App
42	1661.4	98.1	1679	6	US-10-121-055-375 Sequence 375, App
43	1661.4	98.1	1679	6	US-10-121-055-375 Sequence 375, App
44	1661.4	98.1	1679	6	US-10-121-059-375 Sequence 375, App
45	1661.4	98.1	1679	6	US-10-124-822-375 Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-978-403A-522
; Sequence 522, Application US/09978403A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US/09/978,403A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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3	PRIOR FILING DATE: 1998-03-11
4	PRIOR APPLICATION NUMBER: 60/077649
5	PRIOR FILING DATE: 1998-03-11
6	PRIOR APPLICATION NUMBER: 60/077791
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8	PRIOR APPLICATION NUMBER: 60/078004
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10	PRIOR APPLICATION NUMBER: 60/078886
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20	PRIOR APPLICATION NUMBER: 60/079656
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24	PRIOR APPLICATION NUMBER: 60/079689
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26	PRIOR APPLICATION NUMBER: 60/079663
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29	PRIOR FILING DATE: 1998-03-27
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31	PRIOR FILING DATE: 1998-03-27
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33	PRIOR FILING DATE: 1998-03-30
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35	PRIOR FILING DATE: 1998-03-30
36	PRIOR APPLICATION NUMBER: 60/080105
37	PRIOR FILING DATE: 1998-03-31
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44	PRIOR APPLICATION NUMBER: 60/080327
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70	PRIOR APPLICATION NUMBER: 60/081952
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2	PRIOR FILING DATE: 1998-04-21
3	PRIOR APPLICATION NUMBER: 60/0825655
4	PRIOR FILING DATE: 1998-04-21
5	PRIOR APPLICATION NUMBER: 60/0827040
6	PRIOR FILING DATE: 1998-04-22
7	PRIOR APPLICATION NUMBER: 60/0828004
8	PRIOR FILING DATE: 1998-04-22
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11	PRIOR APPLICATION NUMBER: 60/0827977
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13	PRIOR APPLICATION NUMBER: 60/0827968
14	PRIOR FILING DATE: 1998-04-23
15	PRIOR APPLICATION NUMBER: 60/0833366
16	PRIOR FILING DATE: 1998-04-27
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19	PRIOR APPLICATION NUMBER: 60/0833922
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32	PRIOR FILING DATE: 1998-04-29
33	PRIOR APPLICATION NUMBER: 60/0835599
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59	PRIOR APPLICATION NUMBER: 60/0853399
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63	PRIOR APPLICATION NUMBER: 60/0853233
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67	PRIOR APPLICATION NUMBER: 60/0857000
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: PRIOR FILING DATE: 1998-05-15
 : PRIOR APPLICATION NUMBER: 60/085573
 : PRIOR FILING DATE: 1998-05-15
 : PRIOR APPLICATION NUMBER: 60/085704
 : PRIOR FILING DATE: 1998-05-15
 : PRIOR APPLICATION NUMBER: 60/085697
 : PRIOR FILING DATE: 1998-05-15

Query Match	98.1%;	Score 1661.4;	DB 5;	Length 1679;
Best Local Similarity	99.9%;	Pred. No. 1.6e-273;		
Matches 1673; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1;

QY	1	gtccctcagcaaaaacagctggatttaaattctctctgacaaagcttgaagcacaacatct	60
Db	6	gtccctcagcaaaaacagctggatttaaattctctctgacaaagcttgaagcacaacatct	65
QY	61	atcaggaagaagaaaagaaaaaaacccgaaacctgacaaaaaagaagaagaagaaga	120
Db	66	atcaggaagaagaagaag-aaaaaacccgaaacctgacaaaaaagaagaagaagaaga	124
QY	121	aaaaaaatcatgaaaaacccatccagccaaaaaatgacaattctatctcttggcaatctc	180
Db	125	aaaaaaatcatgaaaaacccatccagccaaaaaatgacaattctatctcttggcaatctc	184
QY	181	acggggtgctgtctctgtctcttccaagagatgcccgtgcagcggagatgccacc	240
Db	185	acggggtgctgtctctgtctcttccaagagatgcccgtgcagcggagatgccacc	244
QY	241	ttcccctaaagctatgacaaacgtgacagctccgcgaggggagagcgccacccttagtgc	300
Db	245	ttcccctaaagctatgacaaacgtgacagctccgcgaggggagagcgccacccttagtgc	304
QY	301	actattgacaaacccgggttcaacccgggtggtcctgtgtctaaacccgacaccatctctatgct	360
Db	305	actattgacaaacccgggttcaacccgggtggtcctgtgtctaaacccgacaccatctctatgct	364
QY	361	ggggaatgacaaagtgtgtgccttgatccttcgctgtgtctcttctagcaacccccaaacgcag	420
Db	365	ggggaatgacaaagtgtgtgccttgatccttcgctgtgtctcttctagcaacccccaaacgcag	424
QY	421	tacagcatcgagatccagaaacgtgtagtgtatgacgagggcccctaacacctgctcggtg	480
Db	425	tacagcatcgagatccagaaacgtgtagtgtatgacgagggcccctaacacctgctcggtg	484
QY	481	cagacagacaaaccccaaaagaacctctaggtgtccacctcatgtgtgcaagtatctcccaaa	540
Db	485	cagacagacaaaccccaaaagaacctctaggtgtccacctcatgtgtgcaagtatctcccaaa	544
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Db	545	attgtagagatttcttcagatatctccatlaatgaaggaacaatatatagcctcacctgc	604
QY	601	atagcaactgtagaccagagcgctacggttacttggagacacatctctcccaaagcggtt	660
Db	605	atagcaactgtagaccagagcgctacggttacttggagacacatctctcccaaagcggtt	664
QY	661	ggcttgtgtgagtgaagacgaataacttggaaatccagggcatcacccgggagcagtcaggg	720
Db	665	ggcttgtgtgagtgaagacgaataacttggaaatccagggcatcacccgggagcagtcaggg	724
QY	721	gactacgagtgcagtgcctccaatgacgtgcccgcgcctgtgtacggagagtaaaagtc	780
Db	725	gactacgagtgcagtgcctccaatgacgtgcccgcgcctgtgtacggagagtaaaagtc	784
QY	781	accgtgaactatccacacatacatctcagaagccaaggtacaggtgtccccgtggygacaa	840
Db	785	accgtgaactatccacacatacatctcagaagccaaggtacaggtgtccccgtggygacaa	844
QY	841	aaggggacactgcaagtgtgaagcctcagcaggtccctcagcagaattccagtggtacaag	900
Db	845	aaggggacactgcaagtgtgaagcctcagcaggtccctcagcagaattccagtggtacaag	904
QY	901	gatgacaaaagactgatttgaagggaaaaagaaagqgttgaaggtgaaaaacagacctttcttc	960

Db	905	gatgacacaaagactgattggaagaaaggggtgaagtgtgaaacagacaccttctc	964
QY	961	tcaaaactcatcttcttccaatgtctctcgaacatggaactaacttgctgtgcc	1020
Db	965	tcaaaactcatcttcttccaatgtctctgaacatggaactaacttgctgtgcc	1024
QY	1021	tccaacaagctyggccaacccaatgtccagcatcatbctatttgttccaggcgccgtcagc	1080
Db	1025	tccaacaagctyggccaacccaatgtccagcatcatbctatttgttccaggcgccgtcagc	1084
QY	1081	gaagtgaagcaacgycagcgtcagagagggcaggtctgcgtctgtgctgcctctctgtgc	1140
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QY	1141	ttgcaccctgtctcctcaaattttgatgtgtgagtgccacttccccaccgggaaagctgcgg	1200
Db	1145	ttgcaccctgtctcctcaaattttgatgtgtgagtgccacttccccaccgggaaagctgcgg	1204
QY	1201	ccaccacccaccacccaacacaacagcatgtgcacacaccgcagcaaccaatcagatatata	1260
Db	1205	ccaccacccaccacccaacacaacagcatgtgcacacaccgcagcaaccaatcagatatata	1264
QY	1261	caaatgaaatttagaagaagaacacacagcctcatgtggacacaaatttgaaggaggggaacaaag	1320
Db	1265	caaatgaaatttagaagaagaacacacagcctcatgtggacacaaatttgaaggaggggaacaaag	1324
QY	1321	aatactttggggggaaaaaagtttaaaaaaagaattgaaatlgccttgagatattta	1380
Db	1325	aatactttggggggaaaaaagtttaaaaaaagaattgaaatlgccttgagatattta	1384
QY	1381	ggtacaatggaatttctcttcccaaacgggaagaacacacagcacaccggcttggaacca	1440
Db	1385	ggtacaatggaatttctcttcccaaacgggaagaacacacagcacaccggcttggaacca	1444
QY	1441	ctgcgaagctgcacgtctgcaacaccttttggtgccaggtgtggccaagggtcagcctctctg	1500
Db	1445	ctgcgaagctgcacgtctgcaacaccttttggtgccaggtgtggccaagggtcagcctctctg	1504
QY	1501	cccaacagagtgcgccccaactgtgaaacattcttgagctgtgccaatccaattcaatcagttcc	1560
Db	1505	cccaacagagtgcgccccaactgtgaaacattcttgagctgtgccaatccaattcaatcagttcc	1564
QY	1561	atagaaacgaaacagaatgagaccttccgcggcccaagcgttggcgtgcgggcacatttgtag	1620
Db	1565	atagaagacgaaacagaatgagaccttccgcggcccaagcgttggcgtgcgggcacatttgtag	1624
QY	1621	actgtgccaacccacgcgtgtgtgtgtgtaaacgttgaataaaaaagagcaaaaa	1675
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RESULT 2
US-09-978-544A-522
; Sequence 522, Application US/09978544A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC13
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US/09/978,544A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 181 acggggtgctgtctgttctcttccaagagtgccgtgcgacgagagatgcccac 240
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaud, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C18
; CURRENT APPLICATION NUMBER: US/09/978,681A
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;; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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RESULT 4

US-09-978-757A-522
Sequence 522, Application US/09978757A

GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavira, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978,757A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30

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; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 61 atcaggyaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
Db 66 atcaggyaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124
QY 121 aaaaaaatcatgaanaaccatccagccaanaaatgacaaattctatctcttgygcaattctc 180
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QY 181 acggggctgctgctctgtgtctcttcgaaggagtgcccggtgcagcgagatggcaacc 240
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QY 361 gggaatgacaagtgtgtccttgatctcgcgctgtgtccttcgaagcaaccacaagcag 420
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RESULT 5

US-09-978-564A-522

; Sequence 522, Application US/09978564A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: KJlavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC25

; CURRENT APPLICATION NUMBER: US/09/978, 564A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

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; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

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Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
 Best Local Similarity 99.9%; Pred. No. 1.6e-273;
 Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124
QY 121 aaaaaaatcatgaaacccatccagccaaatgcaaatctatctcttggcaatctc 180
Db 125 aaaaaaatcatgaaacccatccagccaaatgcaaatctatctcttggcaatctc 184
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Db 185 acggggtgctgtctgtctcttccttcaggaagtgcccggtgcagcggaatgcacc 244
QY 241 ttccccaagaagctatgacacagtgacggtcccggaaggggagagcgccaccctcagtg 300
Db 245 ttccccaagaagctatgacacagtgacggtcccggaaggggagagcgccaccctcagtg 304
QY 301 actattgacaacccggtgcaccccggtgctgtgctaaaccgacgacacatctctatgct 360

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Db 305 actattgacacacgggtacacccgggtgcttgcttaaacggcagcaccatcctatgtct 364
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QY 1621 actgtgccaccacggcgtgtgtgtgtgaaacgttgaataaaaaagagcaaaaaaa 1675
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RESULT 6
US-09-999-831A-522
; Sequence 522, Application US/09999831A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C68
; CURRENT APPLICATION NUMBER: US/09/999,831A
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-831A-522

Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Db 6 gtocctcagcaaacagtgatttaaatctccttgcacaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaaaaaacccgaacctgacaaaaaagaagaagaaga 120

Db	66	atcaggaagaagaaag-aaaaaaccgaaacctgacaaaaagaagaaga	124
QY	121	aaaaaaaaatcatgaaaaacatccagccaaaaatycaaatctatctcttggcaatcttc	180
Db	125	aaaaaaaaatcatgaaaaacatccagccaaaaatycaaatctatctcttggcaatcttc	184
QY	181	acgggctgctgtctgtgtctcttccaaaggagtgcccgtcgcagcgagatgccaac	240
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QY	241	ttccccaaagctatygacaacgctgacggtccggcagggggagagcgccacctcagttgc	300
Db	245	ttccccaaagctatygacaacgctgacggtccggcagggggagagcgccacctcagttgc	304
QY	301	actattgacaacccgggtcacccgggtgctgcctgctaaccgcagcaccatctctatgct	360
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QY	361	gggaatgacaagctggtgctgtagtcctgcgcgtgtcctctcagcaaacacc-aaacycag	420
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QY	421	tacagcatcgagatccagaacgtggtgtatgacgagggcccttacacctgtcgtgtg	480
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QY	1141	ttgcacctgtcttccaattttgagtgtgagtgccacttccccaccgggaaaggctgcgcg	1200
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QY	1201	ccaccaccaccaccaccaccacacacacagcaatgtgccaacaccgacagcaacccaatcagatatata	1260
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QY	1441	ctgcgaagctgcacatcggtgcaacctcttgtgtgccaagtgtggccaagggctcaagcctctgtg	1500
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QY	1561	atagagacgaaacagaaatgagacctccgycgccaaagcgtggcgctgcgggcaacttggtag	1620
Db	1565	atagagacgaaacagaaatgagacctccgycgccaaagcgtggcgctgcgggcaacttggtag	1624
QY	1621	actgtgcacaccacgycgtgtgttgtgaaacgttgaataataaaagacaacaaaaa	1675
Db	1625	actgtgcacaccacgycgtgtgttgtgaaacgttgaataataaaagagcaacaaaaa	1679

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RESULT 7
US-09-999-829A-522
; Sequence 522, Application US/09999829A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C61
; CURRENT APPLICATION NUMBER: US/09/999, 829A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522

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; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-829A-522

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Query Match	98.18;	Score 1661.4;	DB 5;	Length 1679;
Best Local Similarity	99.98;	Pred. No. 1.6e-273;		
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				Gaps 1;

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QY	1321	aatacttgggggggaaaaaagttttaaaaaagaatttgaanaatttgccctggcagatattta	1380
Db	1325	aatacttgggggggaaaaaagttttaaaaaagaatttgaanaatttgccctggcagatattta	1384
QY	1381	ggtacaatgtgagtttcttcttcccaaacggggagaacacacagcacaccccggtttgaccca	1440
Db	1385	ggtacaatgtgagtttcttcttcccaaacggggagaacacacagcacaccccggtttgaccca	1444
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QY	1501	cccacagagtgcccccaacgttggaacattctgagctgcccattcccaattcaatcagtcoc	1560
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QY	1561	atagagacgaacagaaatgagaccttccggcccgaagcgtggtgcgtgcgggcactttgtag	1620
Db	1565	atagagacgaacagaaatgagaccttccggcccgaagcgtggtgcgtgcgggcactttgtag	1624
QY	1621	actgtgccaccacggcgctgtgtgtgtgaaacgtgaataataaaagagcaaaaaaaa	1675
Db	1625	actgtgccaccacggcgctgtgtgtgtgaaacgtgaataataaaagagcaaaaaaaa	1679

RESULT 8
US-09-978-375A-522
; Sequence 522, Application US/09978375A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C24
CURRENT APPLICATION NUMBER: US/09/978, 375A
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 522
LENGTH: 1679
TYPE: DNA
ORGANISM: Homo sapiens
US-09-978-375A-522

Query Match 98.1%; Score 1661.4; DB 5; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 61 atcagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 120
Db 66 atcagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 124
QY 121 aaaaatcatgaaacatccagccaaatgacaaatctatctcttgaggcaatctc 180
Db 125 aaaaatcatgaaacatccagccaaatgacaaatctatctcttgaggcaatctc 184
QY 181 acggggtgctgctctgtgtctcttccaaaggagtgcccggtgcgagcgagatgccacc 240
Db 185 acggggtgctgctctgtgtctcttccaaaggagtgcccggtgcgagcgagatgccacc 244
QY 241 tcccccaagctatgacaaacgtgacggtccggcaggggagagcgccaccctcaggtgc 300
Db 245 tcccccaagctatgacaaacgtgacggtccggcaggggagagcgccaccctcaggtgc 304
QY 301 actatlgacaacgggtgcacccgggtggtccttgtaaacggcagccaccctcctatgct 360
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RESULT 9
US-09-978-423A-522
; Sequence 522, Application US/09978423A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
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Query Match 98.1%; Score 1661.4; DB 5; Length 1679;

Best Local Similarity 99.9%; Pred. No. 1.6e-273;

Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 66 atcaggaagaagaag-aaaaaaaccgaacctgacaaaaaagaagaagaagaaga 124
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 6; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtccctcagcaaaacagtgatctaataatctcctcagcaaaagcttgagagcaacaatct 60
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Db 6 gtccctcagcaaaacagtgatctaataatctcctcagcaaaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
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Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124
QY 121 aaaaaaatcatgaaaaaacatccagccaaaaaatgcaaatcttatctcttggaatcttc 180
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Db 125 aaaaaaatcatgaaaaaacatccagccaaaaaatgcaaatcttatctcttggaatcttc 184
QY 181 acgggctgtgctgtctgtctgtctcctcagaagagtgcccgctgcgagcgagagatgccacc 240
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Db 185 acgggctgtgctgtctgtctgtctcctcagaagagtgcccgctgcgagcgagagatgccacc 244
QY 241 ttccccaagctatggaacaacggtccggcgaggggagagcgccaccctcagtgtc 300
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Db 245 ttccccaagctatggaacaacggtccggcgaggggagagcgccaccctcagtgtc 304
QY 301 actattgcaaccgggtcacccgggtgctgctgctaaccgcagcaaccatctctatgct 360
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Db 305 actattgcaaccgggtcacccgggtgctgctgctaaccgcagcaaccatctctatgct 364
QY 361 gggaatgacaagtgtgtcctgtgatacctcgtgtcctctgagcaacaaccaaacgag 420
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Db 365 gggaatgacaagtgtgtcctgtgatacctcgtgtcctctgagcaacaaccaaacgag 424
QY 421 tacagcatcgagatccagaacgttgatgtgtatgacgagggcccttacacctgtcgtgt 480
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Db 425 tacagcatcgagatccagaacgttgatgtgtatgacgagggcccttacacctgtcgtgt 484
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QY 541 atgtagagattcttcagatatctccatataatgaaggaacaataltagcctcactgc 600
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QY 601 atagcaactgtagaccagagcctcactgttagagagacacatctctccaaagcggtt 660
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QY	961	tcaaaactatctctcttcaatgtctctgaacatgactatgggaactacacttgcgtgcc	1020
Db	965	tcaaaactatctctcttcaatgtctctgaacatgactatgggaactacacttgcgtgcc	1024
QY	1021	tccaacaagctgggccaacccaatgccaacatcatgtctatttgtccagggcgcgtcaggc	1080
Db	1025	tccaacaagctgggccaacccaatgccaacatcatgtctatttgtccagggcgcgtcaggc	1084
QY	1081	gaggtgagcaacgcgcacgtccgaggaggcgccagctgcgtctgtctgcctctctgttc	1140
Db	1085	gaggtgagcaacgcgcacgtccgaggaggcgccagctgcgtctgtctgcctctctgttc	1144
QY	1141	ttgcacactgctctccaattttgtatgtgagtgccaacttccccacccgggaaaggctgcgcg	1200
Db	1145	ttgcacactgctctccaattttgtatgtgagtgccaacttccccacccgggaaaggctgcgcg	1204
QY	1201	ccaccaccacccaccacaacacagcaatgagcaacaccgacagcaaccaatcagatatata	1260
Db	1205	ccaccaccacccaccacaacacagcaatgagcaacaccgacagcaaccaatcagatatata	1264
QY	1261	caaatgaaattagaagaacaacacagcctcatgtggagcagaatttgagggagggaacaag	1320
Db	1265	caaatgaaattagaagaacaacacagcctcatgtggagcagaatttgagggagggaacaag	1324
QY	1321	aatacttgggggggaaaaaagttttaaaaaaagaatttgaataattgccttgacatattta	1380
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QY	1561	atagagacgaaacagaaatgagaccttccggcccaagcgttgccgctgcgggcacatttgtag	1620
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QY	1621	actgtgccaacccacgcgctgtgtgtgtgaacacgtgaataataaaagagcaaaaaaaa	1675
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RESULT 11
US-10-013-929A-522
; Sequence 522, Application US/10013929A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

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1  APPLICANT: Paoni, Nicholas F.
2  APPLICANT: Roy, Margaret Ann
3  APPLICANT: Shelton, David L.
4  APPLICANT: Stewart, Timothy A.
5  APPLICANT: Tumas, Daniel
6  APPLICANT: Williams, P. Mickey
7  APPLICANT: Wood, William I.
8  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
9  TITLE OF INVENTION: Acids Encoding the Same
10 FILE REFERENCE: P2630P1C89
11 CURRENT APPLICATION NUMBER: US/10/013,929A
12 CURRENT FILING DATE: 2002-03-19
13 PRIOR APPLICATION NUMBER: 09/918585
14 PRIOR FILING DATE: 2001-07-30
15 PRIOR APPLICATION NUMBER: 60/062250
16 PRIOR FILING DATE: 1997-10-17
17 PRIOR APPLICATION NUMBER: 60/064249
18 PRIOR FILING DATE: 1997-11-03
19 PRIOR APPLICATION NUMBER: 60/065311
20 PRIOR FILING DATE: 1997-11-13
21 PRIOR APPLICATION NUMBER: 60/066364
22 PRIOR FILING DATE: 1997-11-21
23 PRIOR APPLICATION NUMBER: 60/077450
24 PRIOR FILING DATE: 1998-03-10
25 PRIOR APPLICATION NUMBER: 60/077632
26 PRIOR FILING DATE: 1998-03-11
27 PRIOR APPLICATION NUMBER: 60/077641
28 PRIOR FILING DATE: 1998-03-11
29 PRIOR APPLICATION NUMBER: 60/077649
30 PRIOR FILING DATE: 1998-03-11
31 PRIOR APPLICATION NUMBER: 60/077791
32 PRIOR FILING DATE: 1998-03-12
33 PRIOR APPLICATION NUMBER: 60/078004
34 PRIOR FILING DATE: 1998-03-13
35 PRIOR APPLICATION NUMBER: 60/078886
36 PRIOR FILING DATE: 1998-03-20
37 PRIOR APPLICATION NUMBER: 60/078936
38 PRIOR FILING DATE: 1998-03-20
39 PRIOR APPLICATION NUMBER: 60/078910
40 PRIOR FILING DATE: 1998-03-20
41 PRIOR APPLICATION NUMBER: 60/078939
42 PRIOR FILING DATE: 1998-03-20
43 PRIOR APPLICATION NUMBER: 60/079294
44 PRIOR FILING DATE: 1998-03-25
45 PRIOR APPLICATION NUMBER: 60/079656
46 PRIOR FILING DATE: 1998-03-26
47 PRIOR APPLICATION NUMBER: 60/079664
48 PRIOR FILING DATE: 1998-03-27
49 PRIOR APPLICATION NUMBER: 60/079689
50 PRIOR FILING DATE: 1998-03-27
51 PRIOR APPLICATION NUMBER: 60/079663
52 PRIOR FILING DATE: 1998-03-27
53 PRIOR APPLICATION NUMBER: 60/079728
54 PRIOR FILING DATE: 1998-03-27
55 PRIOR APPLICATION NUMBER: 60/079786
56 PRIOR FILING DATE: 1998-03-27
57 PRIOR APPLICATION NUMBER: 60/079920
58 PRIOR FILING DATE: 1998-03-30
59 PRIOR APPLICATION NUMBER: 60/079923
60 PRIOR FILING DATE: 1998-03-30
61 PRIOR APPLICATION NUMBER: 60/080105
62 PRIOR FILING DATE: 1998-03-31
63 PRIOR APPLICATION NUMBER: 60/080107
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65 PRIOR APPLICATION NUMBER: 60/080165
66 PRIOR FILING DATE: 1998-03-31
67 PRIOR APPLICATION NUMBER: 60/080194
68 PRIOR FILING DATE: 1998-03-31
69 PRIOR APPLICATION NUMBER: 60/080327
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71 PRIOR APPLICATION NUMBER: 60/080328
72 PRIOR FILING DATE: 1998-04-01
73 PRIOR APPLICATION NUMBER: 60/080333

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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 6; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtcctcagcaaacagtgatataatctcttcacaaagcttgagagcaacaatct 60
Db 6 gtcctcagcaaacagtgatataatctcttcacaaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124
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Db 125 aaaaaatcatgaaacatccagccaaatgacaaattctctcttggaatcttc 184
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Db 1565 atagagacgaacagaatgagaccttccggycccaagcgtgycgtgcggygcactttggtag 1624
QY 1621 actgtgccaccacgycgtgtgtgtgtaaaacgtgaataaaaaagagcaaaaaaaa 1675

Db 1625 actgtgccaccacgycgtgtgtgtgtaaaacgtgaataaaaaagagcaaaaaaaa 1679
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RESULT 12
US-10-013-918A-522
; Sequence 522, Application US/10013918A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C77
; CURRENT APPLICATION NUMBER: US/10/013,918A
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656

1	PRIOR FILING DATE: 1998-03-26
2	PRIOR APPLICATION NUMBER: 60/079664
3	PRIOR FILING DATE: 1998-03-27
4	PRIOR APPLICATION NUMBER: 60/079689
5	PRIOR FILING DATE: 1998-03-27
6	PRIOR APPLICATION NUMBER: 60/079663
7	PRIOR FILING DATE: 1998-03-27
8	PRIOR APPLICATION NUMBER: 60/079728
9	PRIOR FILING DATE: 1998-03-27
10	PRIOR APPLICATION NUMBER: 60/079786
11	PRIOR FILING DATE: 1998-03-27
12	PRIOR APPLICATION NUMBER: 60/079920
13	PRIOR FILING DATE: 1998-03-30
14	PRIOR APPLICATION NUMBER: 60/079923
15	PRIOR FILING DATE: 1998-03-30
16	PRIOR APPLICATION NUMBER: 60/080105
17	PRIOR FILING DATE: 1998-03-31
18	PRIOR APPLICATION NUMBER: 60/080107
19	PRIOR FILING DATE: 1998-03-31
20	PRIOR APPLICATION NUMBER: 60/080165
21	PRIOR FILING DATE: 1998-03-31
22	PRIOR APPLICATION NUMBER: 60/080194
23	PRIOR FILING DATE: 1998-03-31
24	PRIOR APPLICATION NUMBER: 60/080327
25	PRIOR FILING DATE: 1998-04-01
26	PRIOR APPLICATION NUMBER: 60/080328
27	PRIOR FILING DATE: 1998-04-01
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32	PRIOR APPLICATION NUMBER: 60/081070
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34	PRIOR APPLICATION NUMBER: 60/081049
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37	PRIOR FILING DATE: 1998-04-08
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39	PRIOR FILING DATE: 1998-04-08
40	PRIOR APPLICATION NUMBER: 60/081203
41	PRIOR FILING DATE: 1998-04-09
42	PRIOR APPLICATION NUMBER: 60/081229
43	PRIOR FILING DATE: 1998-04-09
44	PRIOR APPLICATION NUMBER: 60/081955
45	PRIOR FILING DATE: 1998-04-15
46	PRIOR APPLICATION NUMBER: 60/081817
47	PRIOR FILING DATE: 1998-04-15
48	PRIOR APPLICATION NUMBER: 60/081819
49	PRIOR FILING DATE: 1998-04-15
50	PRIOR APPLICATION NUMBER: 60/081952
51	PRIOR FILING DATE: 1998-04-15
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54	PRIOR APPLICATION NUMBER: 60/082568
55	PRIOR FILING DATE: 1998-04-21
56	PRIOR APPLICATION NUMBER: 60/082569
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62	PRIOR APPLICATION NUMBER: 60/082700
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1	PRIOR APPLICATION NUMBER: 60/0834935
2	PRIOR FILING DATE: 1998-04-29
3	PRIOR APPLICATION NUMBER: 60/0834966
4	PRIOR FILING DATE: 1998-04-29
5	PRIOR APPLICATION NUMBER: 60/0834999
6	PRIOR FILING DATE: 1998-04-29
7	PRIOR APPLICATION NUMBER: 60/0835455
8	PRIOR FILING DATE: 1998-04-29
9	PRIOR APPLICATION NUMBER: 60/0835554
10	PRIOR FILING DATE: 1998-04-29
11	PRIOR APPLICATION NUMBER: 60/0835588
12	PRIOR FILING DATE: 1998-04-29
13	PRIOR APPLICATION NUMBER: 60/0835599
14	PRIOR FILING DATE: 1998-04-29
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16	PRIOR FILING DATE: 1998-04-29
17	PRIOR APPLICATION NUMBER: 60/0837422
18	PRIOR FILING DATE: 1998-04-30
19	PRIOR APPLICATION NUMBER: 60/0843666
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25	PRIOR APPLICATION NUMBER: 60/0846377
26	PRIOR FILING DATE: 1998-05-07
27	PRIOR APPLICATION NUMBER: 60/0846399
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31	PRIOR APPLICATION NUMBER: 60/0845988
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37	PRIOR APPLICATION NUMBER: 60/0846433
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41	PRIOR APPLICATION NUMBER: 60/0853388
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43	PRIOR APPLICATION NUMBER: 60/0853233
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50	PRIOR FILING DATE: 1998-05-15
51	PRIOR APPLICATION NUMBER: 60/0855799
52	PRIOR FILING DATE: 1998-05-15
53	PRIOR APPLICATION NUMBER: 60/0855800
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55	PRIOR APPLICATION NUMBER: 60/0855733
56	PRIOR FILING DATE: 1998-05-15
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59	PRIOR APPLICATION NUMBER: 60/0856977
60	PRIOR FILING DATE: 1998-05-15

Query Match	98.1%;	Score 1661.4;	DB 6;	Length 1679;
Best Local Similarity	99.9%;	Pred. No. 1.6e-273;		
Matches 1673;	Conservative	0;	Mismatches	1;
			Indels	1;
			Gaps	1;

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Db 6 gtcccttcagcaaaacagctgcatltaatctccttcgcacaagcttgagcaacacatct 65
QY 61 atcaggaagaagaagaaaaaaacccgaacctgacaaaaaagaagaagaaga 120
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Db 66 atcaggaagaagaagaag-aaaaaacccgaacctgacaaaaaagaagaagaagaaga 124

QY 121 aaaaaatcatgaaaacccatccagccaaaatgcaaatcttatctcttgygcaatcttc 180
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Db 125 aaaaaaatcatgaaaacccatccagccaaaatgcaaatcttatctcttgygcaatcttc 184
QY 181 acggggctgtgctgtctgtgtctcttccaaggagtgcccgctgcgcagcggaatgcccacc 240
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Db 185 acggggctgtgctgtctgtgtctcttccaaggagtgcccgctgcgcagcggaatgcccacc 244
QY 241 ttccccaagctatygacaacgltgaacggtccggcaggggagagcgccaccctcaggtgc 300
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Db 245 ttccccaagctatygacaacgltgaacggtccggcaggggagagcgccaccctcaggtgc 304
QY 301 actatygacaacgggtcaccgggtggtgctggtctaaaccgacgacacatctctatgct 360
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Db 305 actatygacaacgggtcaccgggtggtgctggtctaaaccgacgacacatctctatgct 364
QY 361 gggaatgacaagtggtgctggtgatccctcgctgtgtccttctgagcaaaccccaacgag 420
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Db 365 gggaatgacaagtggtgctggtgatccctcgctgtgtccttctgagcaaaccccaacgag 424
QY 421 taacgcatcgagatccagaacgltgagatglatgacgagggcccttaacactgctcggtg 480
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Db 425 taacgcatcgagatccagaacgltgagatglatgacgagggcccttaacactgctcggtg 484
QY 481 cagaacagacaaccccaaaagacctctgaggtccaacctatgtgcaagtatctcccaaa 540
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Db 485 cagaacagacaaccccaaaagacctctgaggtccaacctatgtgcaagtatctcccaaa 544
QY 541 atgtgagagattcttcagatatctccatgaatgaagggaacataattagcctcacctgc 600
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Db 545 atgtgagagattcttcagatatctccatgaatgaagggaacataattagcctcacctgc 604
QY 601 atagcaactgtgtagaccaagcctacggttactgtgagacacatctctcccaagcggtt 660
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Db 605 atagcaactgtgtagaccaagcctacggttactgtgagacacatctctcccaagcggtt 664
QY 661 ggcttltgtgagtgaaagacgaataacttggaataattcagggtacacccgggagcagtcagg 720
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Db 665 ggcttltgtgagtgaaagacgaataacttggaataattcagggtacacccgggagcagtcagg 724
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Db 725 gactacgagtgagtgccctccaatgacgtgcgcgcgcgtgtgtaacgagagtaaggtc 784
QY 781 accgtgaactatccaccataatttcagaagccaaggtgtacaggtgtcccgctgagacaa 840
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Db 785 accgtgaactatccaccataatttcagaagccaaggtgtacaggtgtcccgctgagacaa 844
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QY 901 gatgacaaaagactgattgaaggaaagagggtgaagtggaanaacagaccttccctc 960
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Db 905 gatgacaaaagactgattgaaggaaagagggtgaagtggaanaacagaccttccctc 964
QY 961 tcaaaactcatcttcttcaagtgctctgaaacatgactatggggaactaacttgctggcc 1020
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Db 965 tcaaaactcatcttcttcaagtgctctgaaacatgactatggggaactaacttgctggcc 1024
QY 1021 tccaacaagctgggccaacccaatgccaagcatcatgtctattgtccagggcgccgtcagc 1080
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Db 1025 tccaacaagctgggccaacccaatgccaagcatcatgtctattgtccagggcgccgtcagc 1084
QY 1081 gaggtgagcaacgacgltcagaggagggcagggctgcgtgctgctcctctctgtc 1140
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Db 1085 gaggtgagcaacgacgltcagaggagggcagggctgcgtgctgctcctctctgtc 1144
QY 1141 ttgcaactgcttctcaaatlttgatgtgagtgccacttcccaacccgggaaaggtgcg 1200
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Db 1145 ttgcaactgcttctcaaatlttgatgtgagtgccacttcccaacccgggaaaggtgcg 1204
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Db 1205 ccaccaccaccaccacacacacagcaatlgcaacaccgcagcaaccaatcagatatata 1264
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Db 1265 caaatgaattagaagaacaacacagcctcatlgggacagaatlttgaggagggaacaag 1324
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Db 1325 aatacttggggggaanaaaagttttaanaagaatltgaaatltgacctgtgcagatatla 1384
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QY 1501 cccacagagtgcccccagctggaacattctgagctggccatcccaatccaatcagctcc 1560
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Db 1505 cccacagagtgcccccagctggaacattctgagctggccatcccaatccaatcagctcc 1564
QY 1561 atagagacgaacagaatygagaccttccggcccaagcgtggtgcgtgcggcacttgtag 1620
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Db 1565 atagagacgaacagaatygagaccttccggcccaagcgtggtgcgtgcggcacttgtag 1624
QY 1621 actgtgcccaacggcgctgtgtgtgtaaaacgtgaaataaaaagagcaaaaaaa 1675
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Db 1625 actgtgcccaacggcgctgtgtgtgtaaaacgtgaaataaaaagagcaaaaaaa 1679

RESULT 13
US-10-017-082A-522
; Sequence 522, Application US/10017082A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C71
; CURRENT APPLICATION NUMBER: US/10/017, 082A
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

[illegible]

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 6; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 6 gtccctcagcaaaacagtgatttaattctccttgccaaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124
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Db 125 aaaaaaatcctgaaaaacccagcccaaaaatgcaaaaattctatctctggcaatctc 184
QY 181 acgggctgctgctctgtctctctccaaagagtgcccgtagcgagagatgcaacc 240
Db 185 acgggctgctgctctgtctctctccaaagagtgcccgtagcgagagatgcaacc 244
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Db 425 tacagcatcagatccagaacgctgtagtgtatgacagagggcccttacacctgtctcgtg 484
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QY 1261 caaatgaaattagaagaacaacacagcctcatgaggagaaatttgaaggaggggaaacaag 1320
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QY 1441 ctgcaagctgcacgtgcgaacacctcttgggtggtgcaggtgtggcagggtcagcctctcgt 1500
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QY 1621 actgtgccaccacggcggtgtgtgtgtgaaacggtgaaataaaagagcaaaaaaa 1675
Db 1625 actgtgccaccacggcggtgtgtgtgtgaaacggtgaaataaaagagcaaaaaaa 1679

RESULT 14
US-10-119-480-125
; Sequence 125, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.


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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 125
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-125

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Query Match      98.1%; Score 1661.4; DB 6; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 6 gtccttcagcaaaaacagtgatattaaatctccttgcaacaagcttgagagcaacaatct 65
QY 61 atcaggaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 120
Db 66 atcaggaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 124
QY 121 aaaaaaatcatgaaacccaatccagccaaaatgcaaatctatctcttgggcaatcttc 180
Db 125 aaaaaaatcatgaaacccaatccagccaaaatgcaaatctatctcttgggcaatcttc 184
QY 181 acgggctggtgctgtctgtctcttccaagaggtgcccgtgcagcgagagatgccacc 240
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QY 241 ttccccaagctatgacaacagtcgctccggcaggggagagcgccaccctcagtgctc 300
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QY 301 actattgcaaacccggtcaccgggtgctgtgttaaacccgagcaccatctctatgct 360
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QY 361 gggaaatgacaagtgtgctgtgattcctcgcgtgtctctctagcaaacaccacaacgcag 420
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QY 421 tacagcatcgagatccagaacgtgtgattgtatgacgagggcccttacacgtgctggtg 480
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Db 605 atagcaactggtagaccagagcctacggttacttggagacacatctctcccaagcggtt 664
QY 661 ggctttgtgagtgaaagcaataacttggaaatlcaggggcatcccccggagagcagtcagg 720
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RESULT 15
US-10-121-049-375
; Sequence 375, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 375
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-375
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Query Match 98.1%; Score 1661.4; DB 6; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.6e-273;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 66 atcagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 124
QY 121 aaaaaatcatgaaacacacacacacacacacacacacacacacacacacacacac 180
Db 125 aaaaaatcatgaaacacacacacacacacacacacacacacacacacacacacac 184
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Search completed: July 12, 2002, 00:32:57
Job time: 11080 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2002, 00:25:10 ; Search time 5033.45 Seconds

(without alignments)
7276.880 Million cell updates/sec

Title: US-09-700-397-2
Perfect score: 1693
Sequence: 1 gtccttcagcaaacagtgtg.....aaaaaaaaaaaaaaaaaaaaa 1693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 segs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1693	100.0	1693	28 US-09-700-397-2	Sequence 2, Appli
2	1661.4	98.1	1679	17 US-09-380-138-522	Sequence 522, App
3	1661.4	98.1	1679	34 US-09-918-585A-522	Sequence 522, App
4	1661.4	98.1	1679	36 US-09-978-188A-522	Sequence 522, App
5	1661.4	98.1	1679	36 US-09-978-189-522	Sequence 522, App
6	1661.4	98.1	1679	36 US-09-978-191A-522	Sequence 522, App
7	1661.4	98.1	1679	36 US-09-978-192A-522	Sequence 522, App
8	1661.4	98.1	1679	36 US-09-978-192A-522	Sequence 522, App
9	1661.4	98.1	1679	36 US-09-978-193A-522	Sequence 522, App
10	1661.4	98.1	1679	36 US-09-978-194A-522	Sequence 522, App
11	1661.4	98.1	1679	36 US-09-978-295A-522	Sequence 522, App
12	1661.4	98.1	1679	36 US-09-978-298A-522	Sequence 522, App
13	1661.4	98.1	1679	36 US-09-978-299A-522	Sequence 522, App
14	1661.4	98.1	1679	36 US-09-978-585-522	Sequence 522, App
15	1661.4	98.1	1679	36 US-09-978-585A-522	Sequence 522, App
16	1661.4	98.1	1679	36 US-09-978-608A-522	Sequence 522, App
17	1661.4	98.1	1679	36 US-09-978-608A-522	Sequence 522, App
18	1661.4	98.1	1679	36 US-09-978-643A-522	Sequence 522, App
19	1661.4	98.1	1679	36 US-09-978-643A-522	Sequence 522, App
20	1661.4	98.1	1679	36 US-09-978-665A-522	Sequence 522, App
21	1661.4	98.1	1679	36 US-09-978-697-522	Sequence 522, App
22	1661.4	98.1	1679	36 US-09-978-802A-522	Sequence 522, App
23	1661.4	98.1	1679	36 US-09-978-824-522	Sequence 522, App
24	1661.4	98.1	1679	36 US-09-981-915A-522	Sequence 522, App
25	1661.4	98.1	1679	36 US-09-999-830A-522	Sequence 522, App
26	1661.4	98.1	1679	36 US-09-999-832A-522	Sequence 522, App
27	1661.4	98.1	1679	36 US-09-999-833A-522	Sequence 522, App
28	1661.4	98.1	1679	36 US-09-999-834A-522	Sequence 522, App
29	1661.4	98.1	1679	37 US-10-002-796-103	Sequence 103, App
30	1661.4	98.1	1679	37 US-10-002-967A-522	Sequence 522, App
31	1661.4	98.1	1679	37 US-10-013-922A-522	Sequence 522, App

32	1661.4	98.1	1679	37	US-10-017-191A-522	Sequence 522, App
33	1661.4	98.1	1679	37	US-10-020-445A-522	Sequence 522, App
34	1661.4	98.1	1679	37	US-10-028-072-375	Sequence 375, App
35	1661.4	98.1	1679	37	US-10-066-193-103	Sequence 103, App
36	1661.4	98.1	1679	37	US-10-066-198-103	Sequence 103, App
37	1661.4	98.1	1679	37	US-10-066-203-103	Sequence 103, App
38	1661.4	98.1	1679	37	US-10-066-211-103	Sequence 103, App
39	1661.4	98.1	1679	37	US-10-066-269-103	Sequence 103, App
40	1661.4	98.1	1679	37	US-10-066-273-103	Sequence 103, App
41	1661.4	98.1	1679	37	US-10-066-494-103	Sequence 103, App
42	1661.4	98.1	1679	37	US-10-066-500-103	Sequence 103, App
43	1661.4	98.1	1679	37	US-10-081-056-55	Sequence 55, Appl
44	1625.8	96.0	2012	21	US-09-544-511-5	Sequence 5, Appl
45	1625.8	96.0	2012	36	US-09-965-212-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-700-397-2
; Sequence 2, Application US/09700397
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Novel Polypeptides, cDNA encoding the same, and use of them
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/7700,397
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
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; APPLICANT: Wood, William I.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Yuan, Jean
; APPLICANT: Baker, Kevin P.
; TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2630R1E
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; CURRENT FILING DATE: 1999-08-25
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 PRIOR FILING DATE: 1998-09-11
 NUMBER OF SEQ ID NOS: 538
 SEQ ID NO 522
 LENGTH: 1679

TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-380-138-522

Query Match 98.1%; Score 1661.4; DB 17; Length 1679;
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; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18

Query Match 98.1%; Score 1661.4; DB 34; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtcctcagcaaaacagtgatlttaatctccttgcaacagcttgagagcaacacatct 60
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QY 61 atcaggaagaagaagaagaagaagaacacgaccttgacaaaaagaagaagaaga 120
Db 66 atcaggaagaagaagaagaagaagaacacgaccttgacaaaaagaagaagaaga 124
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Db 125 aaaaaaatcatgaaaacatccagccaaaatgacaaatctatctctggycaatctc 184
QY 181 acgggctgctgtctgtctcttccaagagtgcccgtygcgagcgagatgccaac 240
Db 185 acgggctgctgtctgtctcttccaagagtgcccgtygcgagcgagatgccaac 244
QY 241 ttcccaaaagctatgacaacgtygacggtccgycaggggagagcgccacctcagtyc 300
Db 245 ttcccaaaagctatgacaacgtygacggtccgycaggggagagcgccacctcagtyc 304
QY 301 actattgacaacgggtgacccgggtggtcgtgcttaaacggcagcacatctctatgct 360
Db 305 actattgacaacgggtgacccgggtggtcgtgcttaaacggcagcacatctctatgct 364
QY 361 gggatgacaagtgtgctgcatctcctcgctgtctcttctagcaacacccaaaagcag 420
Db 365 gggatgacaagtgtgctgcatctcctcgctgtctcttctagcaacacccaaaagcag 424
QY 421 tacagcatcgagatccagaacgtygatgtgtatgacgagggcccttacacctgctgctg 480
Db 425 tacagcatcgagatccagaacgtygatgtgtatgacgagggcccttacacctgctgctg 484
QY 481 cagacagacaaccccaagaacgctctaggggtccaacctatgtgcaagtatctcccaa 540
Db 485 cagacagacaaccccaagaacgctctaggggtccaacctatgtgcaagtatctcccaa 544

QY 541 attgtagagatttcttcagatatctccattaatgaagggaacaatatagcctcacctgc 600
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Db 545 attgtagagatttcttcagatatctccattaatgaagggaacaatatagcctcacctgc 604
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Db 605 atagcaactgttagaccagagcctacggttacttgagacacacatctctccaaacggtt 664
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Db 665 ggcttctgtgaagtgaagacaatactctggaaattccaggcatcacccgggagcagtcagg 724
QY 721 gactacgagtgcagtgcctccaatgacgttgcgcgcgcgtgtacgagagataaaggtc 780
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Db 725 gactacgagtgcagtgcctccaatgacgttgcgcgcgcgtgtacgagagataaaggtc 784
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Db 905 gatgacaaaagactgattggaagaaagagggtgaagagtgaaaaaacagaccttctc 964
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Db 965 tcaaaactccttcttcaatgtctctcgaacatgactatggaactacacttgctgtgccc 1024
QY 1021 tccaaacaagctgggccacaaccaaatgcccagcatcatgtatttggtcaggcgccgcagc 1080
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Db 1025 tccaaacaagctgggccacaaccaaatgcccagcatcatgtatttggtcaggcgccgcagc 1084
QY 1081 gaagtgagcaacgycacgtcgaaggaaggcgctgcctcgtcgtcgtcctcttcgtc 1140
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Db 1145 ttgcacctgcttccaattttgatgtgagtgccaattcccaaccgggaaagctgcgcg 1204
QY 1201 ccaccaccaaccaaccaacacagcaatgycacacccgacagcaaccaatcagatatata 1260
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Db 1205 ccaccaccaaccaaccaacacagcaatgycacacccgacagcaaccaatcagatatata 1264
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QY 1621 actgtgccaccacgycgtgtgtgtgtgaacgtgaataaaaaagagcaaaaaaaa 1675

Db 1625 actgtgccaccacgycgtgtgtgtgtgaacgtgaataaaaaagagcaaaaaaaa 1679
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RESULT 4
US-09-978-188A-522
; Sequence 522, Application US/09978188A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC8
; CURRENT APPLICATION NUMBER: US/09/978,188A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 6 gtccctcagcaaacagtgatgtaatctccttgacacaagcttgagagcaacacatct 65
|||||
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
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Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124

QY 121 aaaaaatcatgaaacacatccagccaaatgcaaatctctcttgygcaatcttc 180
 Db 125 aaaaaatcatgaaacacatccagccaaatgcaaatctctcttgygcaatcttc 184
 QY 181 acggggtgctgctctgtctctctccaaagagtgccgctgagcagcgagatgcccac 240
 Db 185 acggggtgctgctctgtctctctccaaagagtgccgctgagcagcgagatgcccac 244
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 Db 305 actatgacaaccgggtcaccgggtgctgctgctaaaccgagcaccatctctatgct 364
 QY 361 gggaatgacaagtgctgctgagatccctcgctgctctctgagcaacacccaaacgag 420
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Db 1205 ccaccaccaccacacacacacagcaatgcaacacggacagcaacacatcagatalata 1264
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RESULT 5
 US-09-978-189-522
 ; Sequence 522, Application US/09978189
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249

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37	PRIOR FILING DATE: 1998-03-27
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39	PRIOR FILING DATE: 1998-03-30
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41	PRIOR FILING DATE: 1998-03-30
42	PRIOR APPLICATION NUMBER: 60/080105
43	PRIOR FILING DATE: 1998-03-31
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68	PRIOR APPLICATION NUMBER: 60/081229
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Query Match	98.1%;	Score 1661.4;	DB 36;	Length 1679;
Best Local Similarity	99.9%;	Pred. No. 1.2e-236;		
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QY	121	aaaaaaatcatgaaaaaccatccagccaanaatgacaaattctatctcttggcaatcttc	180
Db	125	aaaaaaatcatgaaaaaccatccagccaanaatgacaaattctatctcttggcaatcttc	184
QY	181	acgggctgctgctctctgtctcttccaaaggagtgcgccgtgcgcagcggagatgccaacc	240
Db	185	acgggctgctgctctgtctgtctcttccaaaggagtgcgccgtgcgcagcggagatgccaacc	244
QY	241	ttccccaagctatgacacaacgtgacggtccggcaggggagagcgccaccctcaggtgc	300
Db	245	ttccccaagctatgacacaacgtgacggtccggcaggggagagcgccaccctcaggtgc	304
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QY	361	gggaatgacaagtggtgtgcctgtgatacctgcgcgtgtctctctgagcaaacccaacgcag	420
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QY	421	tacagcatcgagatccagaacggtgatatgtatgacgagggccctacacctgtcgtgtg	480
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QY	721	gactacgagtgagtgcttccaatgacgtgcccgcgcctgtgtacggaagtaaaaggtc	780
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QY	781	accgtgaactatccaccatacatattcagaagccaaggttcaggtgtcccggttggagcaa	840

Db	785	accgtgaactatccaccatacatcttcagaagccaaaggttacaggtgtcccccgttggagcaaa	844
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QY	1021	tcacaacagctgggcccacaccaatgcccagcatcatgtctatttgytccagggcgcgtcagc	1080
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QY	1561	atagagacgaacagaatgagaccttccggcccgaagcgtgycgctgcgycacatttgtag	1620
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
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US-09-978-192-522

; Sequence 522, Application US/09978192
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; APPLICANT: Ashkenazi, Avi
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 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC9
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 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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 PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978, 192A
; PRIOR APPLICATION NUMBER: 2001-10-15
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 901 gatgacaaaagactgattgaaagaaagggtgaaagtgtgaaacacagaccttcctc 960

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RESULT 9
US-09-978-193A-522

; Sequence 522, Application US/09978193A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C6

; CURRENT APPLICATION NUMBER: US/09/978,193A

; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
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Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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RESULT 10

US-09-978-194A-522

; Sequence 522, Application US/09978194A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C10

; CURRENT APPLICATION NUMBER: US/09/978, 194A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtcctcagcaaacacagtgatttaattctccttgacaaagcttgagagcaacaatct 60
Db 6 gtcctcagcaaacacagtgatttaattctccttgacaaagcttgagagcaacaatct 65
QY 61 atcaggaaagaaagaaaaaaaccgaaacctgacaaaaaagaagaagaaga 120
Db 66 atcaggaaagaaagaaaaaaaccgaaacctgacaaaaaagaagaagaaga 124
QY 121 aaaaaaatcatgaaaaccatccagccaaaaatgacaattctatctcttggaattctc 180
Db 125 aaaaaaatcatgaaaaccatccagccaaaaatgacaattctatctcttggaattctc 184
QY 181 acgggctgctgtctgtctctctccaaagagtgcccgctgcagcggagatgcacc 240
Db 185 acgggctgctgtctgtctctctccaaagagtgcccgctgcagcggagatgcacc 244
QY 241 tccccaaagctatgacaacagtgacggtccgagggagagggccaccctcaggtgc 300
Db 245 tccccaaagctatgacaacagtgacggtccgagggagagggccaccctcaggtgc 304
QY 301 actattgacaaccgggtccaccgggtggtggttaaccgcagacacatctctatgtct 360
Db 305 actattgacaaccgggtccaccgggtggtggttaaccgcagacacatctctatgtct 364
QY 361 gggaatgacaagtgtgctctgatacctctgcctgcctctcttgagcaacaccccaacgcag 420
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QY 421 taacagcatcagatccagaaacgtgagtgtatgacgaaggcccttaacatctgctcgtg 480
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Db 845 aaggggacactgcagtgtaagcctcagcagtcctccagcagaatccagtgtaacaag 904

QY 901 gatgcaaaaagactgtatgaaggaagaaggggtgaagtggaaaacagaccttctc 960
Db 905 gatgcaaaaagactgtatgaaggaagaaggggtgaagtggaaaacagaccttctc 964
QY 961 tcaaaactcatcttctcaatgtctctgaacatgactatgggaactacacttgctgccc 1020
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QY 1141 ttgcacctgtctcacaatttgatgtgagtgccacttccccacccgggaaagctgcgg 1200
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RESULT 11
US-09-978-295A-522
; Sequence 522, Application US/09978295A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtccttcagcaaaacagtgatttaattccttcagcaaaagcttgagagcaacaatct 60
Db 6 gtccttcagcaaaacagtgatttaattccttcagcaaaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
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QY 121 aaaaaaatcatyaaaaacatccagccaaaaatgcaaatctctcttgygcaatctc 180
Db 125 aaaaaaatcatyaaaaacatccagccaaaaatgcaaatctctcttgygcaatctc 184
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Db 185 acgggctgctgctctgtctcttccaaagagtgcccgtygcagcgagatgcccacc 244
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RESULT 12

US-09-978-298A-522

; Sequence 522, Application US/09978298A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Flivaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC2

; CURRENT APPLICATION NUMBER: US/09/978,298A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 121 aaaaaaatcatyaaaaccatccagccaaaatgacaaatctatctctggcaatctc 180
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Db 125 aaaaaaatcatyaaaaccatccagccaaaatgacaaatctatctctggcaatctc 184
QY 181 acggygctgctctctgttctctccaaaggagtgcccgtygcagcggagatgcccacc 240
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Db 185 acggygctgctctctgttctctccaaaggagtgcccgtygcagcggagatgcccacc 244
QY 241 ttccccaagctatygacaacgtyacggtccgycaggggagcgccaccctcagtygc 300
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QY 301 actattgacaaccggygtcacccggygtgacctgctaaccgcagcaaccatctatgct 360
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Db 305 actattgacaaccggygtcacccggygtgacctgctaaccgcagcaaccatctatgct 364
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RESULT 13

US-09-978-299A-522

; Sequence 522, Application US/09978299A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC3
; CURRENT APPLICATION NUMBER: US/09/978, 299A
; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585
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 ; PRIOR FILING DATE: 1998-05-15

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
 Best Local Similarity 99.9%; Pred. No. 1.2e-236;
 Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 Db 125 aaaaaaatcatgaaaaaacatccagccaaaaatgcaaatctatctctggycaatctc 184
 QY 181 acgggctgctgctctgtgtctctccaaagagtgcccgtycgagcgagatgccaac 240
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Db	785	accgtgaactatccacatatacttcagaagccaaagggtataagtgccccgttggaaca	844
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Db	1085	gaggtgagcaacgycacgctcgaaggaggcagcgctgcgtctgcgtctgcctctctgcgc	1144
QY	1141	ttgcaacctgtcttcaaattttgatgtgagtgccaactccccaccgggaaagcgtccgcg	1200
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QY	1201	ccaccacacccacacacacacacagcaatgycacacaccgcagcaaccaatcagatatata	1260
Db	1205	ccaccacacccacacacacacacagcaatgycacacaccgcagcaaccaatcagatatata	1264
QY	1261	caaatgaatattagaagaacacacagcctcatgycacagaaatttgaggaggggaacaaag	1320
Db	1265	caaatgaatattagaagaacacacagcctcatgycacagaaatttgaggaggggaacaaag	1324
QY	1321	aatactttgggggggaaaaaagttttaaaaaaagaattgaaaaattgccttgcaatathta	1380
Db	1325	aatactttgggggggaaaaaagttttaaaaaaagaattgaaaaattgccttgcaatathta	1384
QY	1381	ggtacaatgtagtttcttccccaacgycgaagaacacacagcacaccgcgcttgaccoca	1440
Db	1385	ggtacaatgtagtttcttccccaacgycgaagaacacacagcacaccgcgcttgaccoca	1444
QY	1441	ctgcaagctgcacatcgtgcaacctcttgggtgccagtggtggcaaggctcagccctctg	1500
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QY	1501	cccacagagtgccccccacgctggaacattctggagctgycgcacatcccaattcaatcagtc	1560
Db	1505	cccacagagtgccccccacgctggaacattctggagctgycgcacatcccaattcaatcagtc	1564
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RESULT 14
US-09-978-585-522
Sequence 522, Application US/099785855
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

```

; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
;
; LENGTH: 1679
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585-522

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Query Match	98.1%;	Score 1661.4;	DB 36;	Length 1679;
Best Local Similarity	99.9%;	Pred. NO. 1.2e-236;		
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QY 61	atcaggaaagaaagaaagaaaaaaacccgaacctgacaaaaaagaaagaaagaaagaa	120		
Db 66	atcaggaaagaaagaaag-aaaaaaaccgaacctgacaaaaaagaaagaaagaaagaa	124		
QY 121	aaaaaaatcatgtaaaaaaccatccagccaaaaatgtcacaaattctatctcttgggcaatcttc	180		
Db 125	aaaaaaatcatgtaaaaaaccatccagccaaaaatgtcacaaattctatctcttgggcaatcttc	184		
QY 181	acggggtctgctgcctctgtgtctcttccaaagtagtgcccgctgcgcagcggagatgcccacc	240		
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Db 245	ttccccaagctatgtgacaaacgtgtacggtccggcagggggagaaagcgccacccttaaggtgc	304		
QY 301	actattgacaaacgggtgtacccgggtgtgacctgtacaaaccggaccacatctctatgtct	360		
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QY 361	gggaatgacaagtggtgcctggatctcctgcgctgtctccttctgtagcaacacccaagaacgacg	420		
Db 365	gggaatgacaagtggtgcctggatctcctgcgctgtctccttctgtagcaacacccaagaacgacg	424		
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Db 905 gatgacaaaagactgattgaaggaaaagaagggtgaagtgaaaacaacagaccttctc 964
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Db 1025 tccaacaagctgggccaacaaccaatggcagcatcatgtattgtccaggccgcgtcagc 1084
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Db 1145 ttgcacctgcttctcaaattttgatgtgagtgccaacttccccaccgggaaaggctgcgc 1204
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Db 1205 ccaccaccaccaccacaacacagcaatgycacaacccgacagcaaccaatcagatatata 1264
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RESULT 15
US-09-978-585A-522
; Sequence 522, Application US/09978585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978, 585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-522

Query Match 98.1%; Score 1661.4; DB 36; Length 1679;
Best Local Similarity 99.9%; Pred. No. 1.2e-236;
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Search completed: July 12, 2002, 00:25:46
 Job time: 13664 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 22:53:23 ; Search time 102.16 Seconds

(without alignments)
4070.649 Million cell updates/sec

Title: US-09-700-397-2

Perfect score: 1693

Sequence: 1 gtccttcagcaaaacagtg.....aaaaaaaaaaaaaa 1693

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	343	20.3	1238	2	US-08-414-657D-3	Sequence 3, Appl1
2	340.6	20.1	924	2	US-08-414-657D-7	Sequence 7, Appl1
3	340.6	20.1	977	2	US-08-414-657D-1	Sequence 1, Appl1
4	340.6	20.1	1014	2	US-08-414-657D-5	Sequence 9, Appl1
5	338.6	20.0	861	2	US-08-414-657D-9	Sequence 6, Appl1
6	338.6	20.0	912	2	US-08-414-657D-6	Sequence 9, Appl1
7	337.4	19.9	945	2	US-08-414-657D-8	Sequence 8, Appl1
8	333.8	19.7	861	2	US-08-414-657D-10	Sequence 10, Appl1
9	303.6	17.9	756	2	US-08-414-657D-17	Sequence 17, Appl1
10	298.2	17.6	756	2	US-08-414-657D-18	Sequence 18, Appl1
11	100	5.9	219	2	US-08-414-657D-11	Sequence 11, Appl1
12	95.2	5.6	219	2	US-08-414-657D-12	Sequence 12, Appl1
13	77.8	4.6	177	2	US-08-414-657D-13	Sequence 13, Appl1
14	77.8	4.6	177	2	US-08-414-657D-14	Sequence 14, Appl1
15	65.6	3.9	198	2	US-08-414-657D-15	Sequence 15, Appl1
16	63.4	3.7	198	2	US-08-414-657D-16	Sequence 16, Appl1
17	51.2	3.0	240	1	US-08-628-417-6	Sequence 6, Appl1
18	49.4	2.9	1117	4	US-09-247-373B-33	Sequence 33, Appl1
19	48.6	2.9	2447	2	US-09-014-969-14	Sequence 14, Appl1
20	48.6	2.9	2674	4	US-09-817-180-1	Sequence 1, Appl1
21	47.6	2.8	1411	4	US-08-964-127-5	Sequence 5, Appl1
22	47.6	2.8	1411	4	US-09-496-692-5	Sequence 5, Appl1
23	46.8	2.8	903	5	PCT-US95-06406A-21	Sequence 21, Appl1
24	46.6	2.8	630	1	US-08-185-414E-1	Sequence 1, Appl1
25	46.6	2.8	1813	4	US-09-071-224-3	Sequence 3, Appl1
26	46.6	2.8	2280	3	US-08-813-150-1	Sequence 1, Appl1
27	46.4	2.7	140	1	US-08-628-417-5	Sequence 5, Appl1

28	46.4	2.7	376	2	US-08-623-906A-18	Sequence 18, Appl1
29	46.2	2.7	1098	3	US-09-248-335-35	Sequence 35, Appl1
30	46.2	2.7	9589	1	US-07-925-695-1	Sequence 1, Appl1
31	46.2	2.7	9589	1	US-07-925-695-2	Sequence 2, Appl1
32	46	2.7	1798	4	US-09-797-906-1	Sequence 1, Appl1
33	45.8	2.7	124	6	5185243-1	Patent No. 5185243
34	45.8	2.7	224	2	US-08-731-272A-26	Sequence 26, Appl1
35	45.8	2.7	257	2	US-08-520-678A-24	Sequence 24, Appl1
36	45.8	2.7	257	4	US-08-897-126-24	Sequence 22, Appl1
37	45.8	2.7	356	2	US-08-520-678A-22	Sequence 22, Appl1
38	45.8	2.7	356	4	US-08-897-126-22	Sequence 22, Appl1
39	45.8	2.7	1641	1	US-08-300-903A-8	Sequence 8, Appl1
40	45.8	2.7	2184	4	US-08-955-918C-1	Sequence 1, Appl1
41	45.8	2.7	9646	3	US-08-811-566-1	Sequence 1, Appl1
42	45.6	2.7	12980	3	US-08-811-566-5	Sequence 5, Appl1
43	45.4	2.7	1051	4	US-09-245-041-10	Sequence 10, Appl1
44	45.4	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl1
45	45.2	2.7	253	2	US-08-520-678A-25	Sequence 25, Appl1

ALIGNMENTS

RESULT 1
US-08-414-657D-3

; Sequence 3, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

APPLICANT: Levitt, Pat

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

APPLICANT: Zhukareva, Victoria

TITLE OF INVENTION: Limbic System-Associated Membrane

TITLE OF INVENTION: Protein and DNA

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,657D

FILING DATE: 31-MAR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1238 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 56...1069

OTHER INFORMATION:

US-08-414-657D-3

Query Match 20.3%; Score 343; DB 2; Length 1238;
Best Local Similarity 62.0%; Pred. No. 6.5e-76;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

QY 201 tctctccaaggagtgcccgctgcgacgagatgccaccttccccaaagtatygacaa 260
DB 121 TCTTCCACAGAGACTGCCCGTTCCGACGCGTGAT-----TTTAACCGAGCGACGACAA 174

QY 261 cgtgacggtccgagcagggagagcgccacctcagtgactatgacaaccggttac 320
DB 175 CATCACCGTGAGGACAGGGGACAGGCCATCCTCAGGTGTGTGTAGAGACAAAGAACTC 234

QY 321 ccggtggtcgtgtgtaaacgcgacacatcctctatgtcgtggaatgacaagtgtgcct 380
DB 235 GAAAGTGGCCCTGTTGAACCGCTTGCAATCTTCCGTGACACGACAAAGTGTCTCT 294

QY 381 ggtatcctcgtgtgtccttctgtgacaaacccaacgcagtaacagatcgatccagaa 440
DB 295 GGACCCCTCGGGTTGAGCTGGAAGAAACGCCATGCTCTGGAATACAGCCCTCCGATCCAGAA 354

QY 441 cgtgatatgtatgacagagggcccttaacactgtcgtgtgcagacagacacaccccaa 500
DB 355 GGTGATGTCTATGATGAAGGATCTTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

QY 501 gaccttaggtgccacctcattgtgcaagtatctcccaaatgttagagattcttcaga 560
DB 415 GACCTTCAAGTTTACTGTATTGTACAAAGTTCACCAAGATCTCCACATCTCCTCGGA 474

QY 561 tatctcaattaatgaagggaaacaatatagcctcaactgcaatagcaactgttagaccaga 620
DB 475 TGTCACTGTGAATGAGGGGACAGCAATGTAACTTGCTGCAATGAGCCAAATGGCGCCCTGA 534

QY 621 gcctacggttacttgagacacatctctcccaagcgtgttgcttgtgagtgaagacga 680
DB 535 ACCTGTATACCTTGAGACACCTTACACACCTTGGAAGAGAAATTTGAAGGAGAGAAGA 594

QY 681 atacttggaattcaaggcatcacccgggagcagtcagggactacgagtgcagtgcctc 740
DB 595 ATATCTGAGATCCTAGGCATCACCGGGAACAGTCAAGCAATATATGATGCAAGGCTGC 654

QY 741 caatgacgtgcccgcgcctgtgtacgagagtaaaaggtcacggtgaactatccacata 800
DB 655 CAACGAGGTCTCCTCCGGGATGTCAACAAGTCAAGGTCACTGTGAATATCCACCCAC 714

QY 801 cattcagaagccaaggttacaggtgtcccccgtggtgacaaaaggggacactgcagtgtga 860
DB 715 CATCACAGAGTCTTAAGAGCAATGAAGCCACACAGGACAGCAAGCTTCCCTCAATGTGA 774

QY 861 agcctcagcagtcacctcagcagaatctcagtggtacaaagatgacaaaagactgtatga 920
DB 775 AGCCTCAGCGGTGCTTGACCTGACTTTGAGTGTGTACCGGGATGACACACAG---GATAAA 831

QY 921 aggaagaagaaggtgtgaagatgtgaacacagaccttccctcacaactcatcttctcaa 980
DB 832 CAGTGCAAAACGGCCTTGAGATTAGAGCACTGAGGGCCAGTCTTCCCTGACGCGTACCAA 891

QY 981 tgtctctgaacatgactatggaactacacttgctggtgcctccaacaagctggtgccaac 1040
DB 892 CGTCACTGAGGAAACACTACAGGCAACTATACCTGTGTGGCTGCCAACAAAGCTCGCGCTCAC 951

QY 1041 caatgcagcatcatgtctattgtgtccagggtccgtcagcgaggtgagcaacggtcac 1100
DB 952 CAATGCCAGCCTAGTCTTTCAGACACCGGGTCCGTGAG--AGGAATCAACGGAATCCAT 1008

QY 1101 gaggagggcaggtcgtctgtgtgtctctcttctgtcttgcaacctgtcttcaatt 1160
DB 1009 CAGTCTGGCCGTACCACTGTGTGGCTGTGTGCGAGCGTCCCTGTCTCTCAGCAATATG 1068

QY 1161 ttgat 1165
DB 1069 TTAAT 1073

RESULT 2
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283

;; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60

;; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543

;; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:

;; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...924
; OTHER INFORMATION:
; US-08-414-657D-7

Query Match 20.1%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 2.3e-75;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 201 tctctccaaggagtgcccgctgcgacgagatgccaccttccccaaagtatygacaa 260
DB 45 TCTTCCACAGGAGACTGCTGTTCGACGCGTGAT-----TTTAACCGAGCGACGACAA 98

QY 261 cgtgacggtccgagcagggagagcgccacctcagtgactatgacaaccggttac 320
DB 99 CATCACCGTGAGGACAGGGGACACAGCCATCCTCAGGTGCGTTTGAAGAGACAAAGAACTC 158

QY 321 ccggtggtcgtgtgtaaacgcgacacatcctctatgtcgtggaatgacaagtgtgcct 380
DB 159 AAAGTGGCCCTGTTGAACCGTCTTGCAATCTTTCGTGACATGACAAAGTGTCTCT 218

QY 381 ggtatcctcgtgtgtccttctgtgacaaacccaacgcagtlacagatcgatccagaa 440
DB 219 GGACCCACGGGTGAGCTGGAAGAAACGCCATTTCTGTGAATACAGCCCTCCGAATCCAGAA 278


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QY 441 cgtgagtgatgacgagggcccttacacctgctcggtgcagacagacaaccacaa 500
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Db 279 GGTGATGTCTATGATGAGGGTCTCTACACTTGTCTCAGTTCAGACACAGCATGAGCCAA 338
QY 501 gacctctagggtccacctcattgtgcaagatattcccaaatgtagagattcttcaga 560
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 GACCTCCCAAGTTTACTTGATCGTACAAAGTCCCAAGATCTCCATATCTCCCTCGA 398
QY 561 tatctccattaatgaagggaacaataattagcctcaacctgcatagcaactgtagaccaga 620
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Db 399 TGTCACTGTGAATGAGGGGACCAACCTGACTCTGTGCTGCATGGCCCAATGGCCCTCTGA 458
QY 621 gcctacggttacttgagacacatctctccaaagcgggttgcttgtagtgaagacga 680
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 459 ACCTGTATTCACCTGGAGACACCTTACACCACTGGAAGGAATTGGAAGGAGAAGA 518
QY 681 atacttgaaattcagggcatcaccgggagcagtcaggggactacagagtgcagtcctc 740
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Db 519 ATATCTGGACATCCTTGGCATCACCAAGGAGCAGTCAAGCAAAATATGATGCAAAAGCTGC 578
QY 741 caatgacgtgcccgcgcctgtgtacgagagtaaaagtcacccgfygaactatccacata 800
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Db 579 CAACGAGGTTCTCTCGGGGATGTCAACAAGTCAAGGTCACCTGTGAATATCTCTCCAC 638
QY 801 cattcagaagccaaggttacaggtgtcccccgtgagacaaaggggacactgcagtgta 860
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Db 639 TATCACAGAAATCCAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCACTCAAAATGTGA 698
QY 861 agcctcagaagtcacctcagcagaattccagtggtacaaaggtacgaagagactgtga 920
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Db 699 GGCCTCGGACGTGCTTGCACCTGACTTGTGAGTGTACCGGATGACACTAG--GATAAA 755
QY 921 aggaagaagggtgaaagtgaagaacagaccttccctcctcaaaactcatcttcca 980
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Db 756 TAGTGCCAATGGCCTTGACATTAAGAGCACGAGGGCCAGTCTTCCCTGACGGTGACCAA 815
QY 981 tgtctctgaacatgactatgtggaactacaacttgctgctcctccaagaagctgggccaac 1040
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Db 816 CGTCACTGAGGAGCACTACGCACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTGCAC 875
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Db 876 CAATGCCAGCCTAGTCTCTTTCAAGACCTGGGTCGGTGAGAG 916

RESULT 3
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210.
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...976
; OTHER INFORMATION:
US-08-414-657D-1
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Query Match 20.1%; Score 340.6; DB 2; Length 977;
Best Local Similarity 63.3%; Pred. No. 2.3e-75;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;
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QY 201 tctctccaagagagtcgccgtgacgagcgcagatgcccacttccccaagctatggacaa 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 46 TCTTCCACAGGACTGCTGTTCGACCGTGGAT-----TTTACCAGAGGACAGGACAA 99
QY 261 cgtgacgtccggcaggggagagagccaccctcaggtgacactatgtgacaacgggtcac 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 CATCACCGTGAGGAGGAGGAGACACAGCCATCTCTCAGGTGCGTTCTTGAAGACAAAGACTC 159
QY 321 ccgggtggtcgttaaacgcgacacacatcctctatgctggtgaatgacaagtgtgct 380
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Db 160 AAAGTGGCCTGGTTGAACCGCTTCTGGCATCATTTTGTGACATGACAAGTGTCTCT 219
QY 381 ggtacctcggtgtgtctcttgagcaacacccaacgcaatgacagatcgagatccagaa 440
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Db 220 GAACCCACGGGTTGAGCTGGAGAAACGCCATCTCTGGAATACAGCCTCCGAATCCAGAA 279
QY 441 cgtgagtgtatgacgagggcccttaacctgtgctggtgcagacagacaaccacaa 500
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Db 280 GGTGATGTCTATGATGAGGGTCTCTACACTTGTCTCAGTTCAGACACAGCATGAGCCCAA 339
QY 501 gacctctagggtccacctcattgtgcaagatattcccaaatgttagagattcttcaga 560
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Db 340 GACCTCCCAAGTTTACTTGATCGTACAACTCCCAAGATCTCCCAATATCTCTCCGGA 399
QY 561 tatctccattaatgaagggaacaataattagcctcaacctgcatagcaactgtagaccaga 620
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Db 400 TGTCACTGTGAATGAGGGGACCAACGTGACTCTGTGTGCAATGGCCATGGCCGTCTGA 459
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Db 460 ACCTGTATTCACCTGGAGACACCTTACACCAACTGGAAGGAATTGGAAGGAGAAGA 519
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Db 580 CAACGAGGTTCTCTCGGGGATGTCAACAAGTCAAGGTCACTGTGAATATCTCTCCAC 639
QY 801 cattcagaagccaaggttacaggtgtcccccgtgagacaaaggggacactgcagtgta 860
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GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...861
OTHER INFORMATION:

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Query Match	20.0%;	Score 338.6;	DB 2;	Length 861;
Best Local Similarity	63.7%;	Pred. No. 6.9e-75;		
Matches 531; Conservative	0;	Mismatches 299;	Indels 3;	Gaps 1;

[illegible]

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Db	384	TGGCCGCTCCTGAACTGTATATCACTGGAGACACCTTACACCAACTGGAAGGAATTGA	443
QY	669	gagtgaagacggaatacttggaaattcagggcatacccgggagcaqtcaagggactaca	728
Db	444	AGGAGAAAGAGATATCTGTGAGATTCCTTGGCATCACCAAGGAGCAGTCAAGCAATATGA	503
QY	729	gtgcagtgccctccaatgacgttggccgcccgtgtacggagagtaaaagttcacccgtgaa	788
Db	504	GTGCAAAAGCTGCCAACGAGGCTCTCCTGGCGGATGTCAAAACAAGTCAAGGTCACTGTGAA	563
QY	789	ctatccaccatacatttcagaagccaagggtacaggtgtccccgttggacaaaaggggac	848
Db	564	CTATCTCTCCCACTATACAGAAATCCAAAGACCATGAAGCCACCACAGGACGACAAGCTTC	623
QY	849	actgcagtggtgaagcctcagcagttccctcagcagaattccaagtygtacaagatgacaa	908
Db	624	ACTCAATATGTAGGCCCTCGGCAAGTGCCTGCACCTTGACTTTGATGTGTACCGGGATGACAC	683
QY	909	aagactgattgaagaaagaaagggttgaagttgaaatgaaacacagacccttctctcaaaact	968
Db	684	TAG---CATTAATAGTGGCCAATGGCCTTGAGATTAAAGACACGAGGAGGCCAAGCTTCCCT	740
QY	969	catctcttcaatgtctcttgaacatgactatggaactacacttgcgttggcctccaaca	1028
Db	741	GACGGGTGACCAACGTCACTGAGGAGCACTACGGCACTACACCTGTGTGGCTGCCAACAA	800
QY	1029	gctgggcacacccaatgcccagcatcatgtatttggttccaggcgcgtcacg	1081
Db	801	GCTGGGGTCAACCAATGCCAGCCTTACTCTTTACAGACCTGGGTTGGGTGAGAG	853

RESULT 6
US-08-414-657D-6
Sequence 6, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414, 657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214


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Db 240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299
QY 441 cgtgagtgtatgacgagggcccttacacctgctcggtgcagacagacaaccacccaaa 500
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Db 300 GGTGATGTCTATGATGAAGATCCTACACATGCTCAGTTCAGACACAGCAAGAGCCCAA 359
QY 501 gacctataggtccacctcatgtgcaaglatctcccaaatgtagagattcttcaga 560
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Db 360 GACCTCTCAGATTACTGTGATTGTACAGAGTTCACCAAGATCTCCACACTCTCCTCGGA 419
QY 561 tatctccattaatgaagggaaacataattagcctcacctgcataagcaactgtagaccaga 620
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Db 420 TGTCACTGTGAATGAGGGCAGCAATGTAACTGCTGCTGCAATGGCCAATGGGCCCTGA 479
QY 621 gcctacggttacttggagacacatctctcccaagcggttggtttgtgagtgaagcga 680
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Db 480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAGAGAGATTGGAAGGAGAGAGAGA 539
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Db 540 ATATCTGGAGATCCTAGGCATCACACGAGGGAACAGTCAAGCAATATGAGTGCAGGCTGC 599
QY 741 caatgacgtggccgcccgtgtgtaacgagtaagtgtaacggtgaactatccacata 800
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Db 600 CAACGAGGTCTCCTCCCGGATGTCAAAACAAGTCAAGGTCACTGTGAATATCCACCCAC 659
QY 801 cattcagaagccaaggttacagtggtcccggtgggacaaaggggacactgagtgta 860
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Db 660 CATCACAGAGTCTAAGACCAATGAAGCCACCAACAGACAGCAAGCTTCCCTCAATGTGA 719
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Db 720 AGCCTCAGCGGTGCTGACCTGACCTGACTTTGAGTGTGACCGGATGACACCAAG--GATAAA 776
QY 921 aggaagaagaaggtgtaaaagtgtgaaacagacatttcctctcaaaactcatcttctcaa 980
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Db 777 CAGTGCAACGGCCTTGAGATTAAAGAGCACTGAGGGCCAGTCTCCTGACGGTACCAAA 836
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Db 837 CGTCACTGAGGAACACTACGCGCAACTATACTGTGTGGCTGCGCAACAAGCTCGCGGTCA 896
QY 1041 caatgccagcatcatgtatttggccaaggcgccgtcagcg 1081
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Db 897 CAATGCCAGCCTAGTCTTTTCAGACCCGGGTGCTGAGAG 937

RESULT 8
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
```

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; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
;
; US-08-414-657D-10

Query Match 19.7%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 1.le-73;
Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

QY 249 agctatgacaacggtgacggtccgaggggagagcgccacctcagtgactattga 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 24 AGGACACGACACAATACACCTGAGGCAAGGGGACACGGCCATCTCAGGTGTGTAGA 83
QY 309 caaccggttcacccggtggtgctgctaaccgagacacatctctatgctgggaatga 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 AGACAAGAACTCGAAGTGGCTGTGTAACCGCTCTGGCATCATCTTGGATATACAGCA 143
QY 369 caagtgtgctgtgacatctcggtgtgctctctctgagcaacacccaaacgcagtaacat 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 CAAGTGTCTCTGGACCTCGGGTGTAGCTGGAGAAACGCCATGCTTGAATATACAGCT 203
QY 429 cgaatccagaacggtgagtgtgtatgacgagggcccttacacctgctcggtgcagacaga 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 CCGAATCCAGAAAGTGGATGTCTATGATGAAGGATCTTACACATGCTCAGTTCAGACACA 263
QY 489 caaccacccaagacctataggttcacacctcatgtgcaaglatctcccaaatgtaga 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 GCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAAGTTCACCAAGATCTCCAA 323
QY 549 gattctcagatatctccattaatgaagggaaacataattagcctcacctgcataagcaac 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 CATCTCCGCGGATGTCACTGTGAATGAGGCGACGACATGTAAACCTGTGCTGCAATGGCCA 383
QY 609 tggtagaccagagcctacggttacttggagacacatctctcccaagcggttggtgtgt 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 TGGGCGCCCTGAACCTGTATTATCACCTTGAGAGACACCTTACACCACTTGAAGAAATTGA 443
QY 669 gagtgaagaagaatacttggaaattcaagggcatcacccgggagcgagtcagggactaaga 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 444 AGGAGAAGAGAATATCTGGAAGATCTTACCATCACCAAGGCAAGGCAATATGA 503
QY 729 gtgcagtgctccaatgacgtggccgcccgtgtgtaacgagtaaaagtcacacgtgaa 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 504 GTGCAAGGCTGCCAAGAGGTCTCCTCCGGGATGTCAAAACAAGTCAAGGTCACTGTGAA 563
QY 789 ctatccacatacatctcagaagccaaggttacagtggtcccggtgggacaaagggagac 848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 564 CTATCCACCAACCATCACAGAGTCTAAGACCAATGAAGCCACACAGGACGACAGACTTC 623
QY 849 actgcagtgtaagcctcagcagtcacctcagcagaattccagtggtgtacaagatgacaa 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 624 CTTCAATATGTAAGCCTCAGCGGTGCTGCTGACACTTGTAGTGTGTAACCGGATGACAC 683
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QY 337 aaccgcagcaccatcctctatgctgggaatgacaaagtgtgctcgtgaccccgctgac 396
|||||
Db 61 AACCGTCTGGCATCATTTTGGCGACATGACAGAGTGTCTCTGGACCCAGGGTTGAG 120
QY 397 ctctgagcaacaccccaacgcagctacagcatcgagatccagaacgctggtatgac 456
|||
Db 121 CTGAGAAACGCCATCTCTGGAATACAGCCCTCCGAATCCAGAGGTGGATGTCTATGAT 180
QY 457 gagggcccttacacctgtcgtgacagaca 488
|||||
Db 181 GAGGTTCTTACACTTGTCTCAGTTTCAGACACA 212

RESULT 12

US-08-414-657D-12
; Sequence 12, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...219
; OTHER INFORMATION:
; US-08-414-657D-12

Query Match 5.6%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 9.1e-15;
Matches 139; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 277 ggggagagcgcaccctcaggtgacattgacaacgcggtcaccgcggtggtgctgcta 336
|||||
Db 1 GGGGACACGCGCATCCTGCTGTGTGTAGAAAGACAGAACTCGAAAGTGGCTGTG 60

QY 337 aaccgcagcaccatcctctatgctgggaatgacaaagtgtgctcgtgaccccgctgac 396
|||||
Db 61 AACCGTCTGGCATCATTTTGGCGACATGACAGAGTGTCTCTGGACCCAGGGTTGAG 120
QY 397 ctctgagcaacaccccaacgcagctacagcatcgagatccagaacgctggtatgac 456
|||
Db 121 CTGAGAAACGCCATGCTCTGGAATACAGCCCTCCGAATCCAGAGGTGGATGTCTATGAT 180
QY 457 gagggcccttacacctgtcgtgacagaca 488
|||||
Db 181 GAAGGATCTTACACATGTCTCAGTTTCAGACACA 212

RESULT 13

US-08-414-657D-13
; Sequence 13, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...177
; OTHER INFORMATION:
; US-08-414-657D-13

Query Match 4.6%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 1.7e-10;
Matches 115; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 577 gggacaatatagcctcaccctgcatagcaactgtgtagaccagagcctaacgttacttg 636
|||||
Db 1 GGCAGACAGCTGACTGTGCTGTGATGCGCAATGCGCGTCTGTAACCTGTATACACCTGG 60

QY 637 agacacatctctcccaagcggttggttgtgaagtgaagacataacttgaataattcag 696
 ||||| | | | | | |||| | |||| | |||| | |||| |
 Db 61 AGACACCTTACACCAACCACTGGAAGGAATTTGAAGGAGAAGAATATCTGGAGATCCTT 120
 QY 697 ggcataccocggagcgagtcaggggactacgagtgcagtgccctcaatgacgtggcc 753
 ||||| | ||||| ||||| | | ||||| | |||| | |||| |
 Db 121 GGCAATACCCAGGGAGCAGTCAGGCAATATGAGTGCAGAAAGCTGCCAACGAGGCTCTCC 177

RESULT 14

```

US-08-414-657D-14
; Sequence 14, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
;   APPLICANT: Levitt, Pat
;   APPLICANT: Pimenta, Aurea
;   APPLICANT: Fischer, Itzhak
;   APPLICANT: Zhukareva, Victoria
;   TITLE OF INVENTION: Limbic System-Associated Membrane
;   TITLE OF INVENTION: Protein and DNA
;   NUMBER OF SEQUENCES: 60
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dechart Price & Rhoads
;   STREET: 997 Lenox Drive, Building 3, Suite 210
;   CITY: Lawrenceville
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08543
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSeq for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/414,657D
;   FILING DATE: 31-MAR-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Bloom, Allen
;   REGISTRATION NUMBER: 29,135
;   REFERENCE/DOCKET NUMBER: 317743-102
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-520-3214
;   TELEFAX: 609-520-3259
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 177 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..177
;   OTHER INFORMATION:
;
US-08-414-657D-14

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Query Match	4.6%;	Score 77.8;	DB 2;	length 177;
Best Local Similarity	65.0%;	Pred. No. 1.7e-10;		
Matches 115; Conservative	0;	Mismatches 62;	Indels 0;	Gaps 0;

[illegible]

DQ 697 ggcattaccocggagcagtcacggygaactacagtgcagtccctccaatgatcgtagcc 753
||||||| |||| | || ||||| || |||| |
Db 121 ggcatcacccagggaacagtacagccaatatatgctgcagaagctgccacaacagagctccc 177

RESULT 15

```

US-08-414-657D-15
; Sequence 15, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...198
; OTHER INFORMATION:
US-08-414-657D-15

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Query Match	3.9%;	Score 65.6;	DB 2;	Length 198;
Best Local Similarity	61.5%;	Pred. No. 1.9e-07;		
Matches 123;	Conservative 0;	Mismatches 74;	Indels 3;	Gaps 1;

QY	835	ggacaaaggagacactgcagtgtgtaagcctcagcagtcctccctcagcagaattccagltg	894
Db	1	GGACGACAAGCTTCACCTCAATGTGAGGCCCTGGGCAGTGGCCTGCACCTGACTTTGAGTGG	60
QY	895	tacaagatgacaaaagactgattgaaagaaagagggtgaaagltgysaaacagacct	954
Db	61	TACCGGATGACACTAG---GATAAATAGTGCCCAATGGCCCTTGAGATTAGAGACACGGAG	117
QY	955	ttccttcaaaactcattcttcttcaatgtctctgacatgactatggaactacacttgc	1014
Db	118	GGCCAGTCTTCCCTGACGGGTGACCACAACGTCACTGAGGAGCACTACGGCAACTACACCTGT	177

QY 1015 gtggcctcacacaagctggg 1034
||||| |||||||||
Db 178 GTGGCTGCCACACAGCTGGG 197

Search completed: July 11, 2002, 22:53:32
Job time: 13221 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 21:28:17 ; Search time 418.18 Seconds

(without alignments)
4155.153 Million cell updates/sec

Title: US-09-700-397-1

Perfect score: 1032

Sequence: 1 atgaataaccatccagccaaa.....tgacactgtcttcaattt 1032

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1156321 seqs, 841861299 residues

Total number of hits satisfying chosen parameters: 2312642

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	1679	5	US-09-978-403A-522 Sequence 522, App
2	1032	100.0	1679	5	US-09-978-544A-522 Sequence 522, App
3	1032	100.0	1679	5	US-09-978-681A-522 Sequence 522, App
4	1032	100.0	1679	5	US-09-978-757A-522 Sequence 522, App
5	1032	100.0	1679	5	US-09-978-564A-522 Sequence 522, App
6	1032	100.0	1679	5	US-09-999-831A-522 Sequence 522, App
7	1032	100.0	1679	5	US-09-999-829A-522 Sequence 522, App
8	1032	100.0	1679	5	US-09-978-375A-522 Sequence 522, App
9	1032	100.0	1679	5	US-09-978-423A-522 Sequence 522, App
10	1032	100.0	1679	6	US-10-013-921A-522 Sequence 522, App
11	1032	100.0	1679	6	US-10-013-929A-522 Sequence 522, App
12	1032	100.0	1679	6	US-10-013-918A-522 Sequence 522, App
13	1032	100.0	1679	6	US-10-017-082A-522 Sequence 522, App
14	1032	100.0	1679	6	US-10-119-480-125 Sequence 125, App
15	1032	100.0	1679	6	US-10-121-050-375 Sequence 375, App
16	1032	100.0	1679	6	US-10-121-050-375 Sequence 375, App
17	1032	100.0	1679	6	US-10-121-053-375 Sequence 375, App
18	1032	100.0	1679	6	US-10-121-043-375 Sequence 375, App
19	1032	100.0	1679	6	US-10-121-044-375 Sequence 375, App
20	1032	100.0	1679	6	US-10-121-047-375 Sequence 375, App
21	1032	100.0	1679	6	US-10-121-054-375 Sequence 375, App
22	1032	100.0	1679	6	US-10-121-056-375 Sequence 375, App
23	1032	100.0	1679	6	US-10-121-057-375 Sequence 375, App
24	1032	100.0	1679	6	US-10-121-058-375 Sequence 375, App
25	1032	100.0	1679	6	US-10-121-060-375 Sequence 375, App
26	1032	100.0	1679	6	US-10-121-063-375 Sequence 375, App

27	1032	100.0	1679	6	US-10-123-108-375 Sequence 375, App
28	1032	100.0	1679	6	US-10-123-154-375 Sequence 375, App
29	1032	100.0	1679	6	US-10-123-156-375 Sequence 375, App
30	1032	100.0	1679	6	US-10-123-157-375 Sequence 375, App
31	1032	100.0	1679	6	US-10-123-212-375 Sequence 375, App
32	1032	100.0	1679	6	US-10-123-213-375 Sequence 375, App
33	1032	100.0	1679	6	US-10-123-109-375 Sequence 375, App
34	1032	100.0	1679	6	US-10-121-041-375 Sequence 375, App
35	1032	100.0	1679	6	US-10-121-045-375 Sequence 375, App
36	1032	100.0	1679	6	US-10-121-046-375 Sequence 375, App
37	1032	100.0	1679	6	US-10-121-051-375 Sequence 375, App
38	1032	100.0	1679	6	US-10-121-040-375 Sequence 375, App
39	1032	100.0	1679	6	US-10-121-052-375 Sequence 375, App
40	1032	100.0	1679	6	US-10-121-061-375 Sequence 375, App
41	1032	100.0	1679	6	US-10-121-042-375 Sequence 375, App
42	1032	100.0	1679	6	US-10-121-055-375 Sequence 375, App
43	1032	100.0	1679	6	US-10-121-059-375 Sequence 375, App
44	1032	100.0	1679	6	US-10-124-822-375 Sequence 375, App
45	1032	100.0	1679	6	US-10-124-822-375 Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-978-403A-522
Sequence 522, Application US/09978403A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaaatgcacaattctatctcttgggcaatcttcagggtg 60
Db 134 atgaaaccatccagccaaaatgcacaattctatctcttgggcaatcttcagggtg 193
QY 61 gctgctctgtctctccaaaggagtcgctgagcgagagatgccacttcccaaa 120
Db 194 gctgctctgtctctccaaaggagtcgctgagcgagagatgccacttcccaaa 253
QY 121 gctatgacaacgtgacggtccggcagggggagagcgccaccctcaggtgcactattgac 180
Db 254 gctatgacaacgtgacggtccggcagggggagagcgccaccctcaggtgcactattgac 313
QY 181 aaccgggtcaccgggtggtgctgctaacaacgcagacccatcctctatgtctgggaatgac 240
Db 314 aaccgggtcaccgggtggtgctgctaacaacgcagacccatcctctatgtctgggaatgac 373
QY 241 aagtggtgctgatactcctcgctgtgtctctctgagcaaccaccaacgcagtaacgcatc 300
Db 374 aagtggtgctgatactcctcgctgtgtctctctgagcaaccaccaacgcagtaacgcatc 433
QY 301 gagatccagaacgtgagatgtatgacgagggcccttaacacctgtcgtgtgcagacagac 360
Db 434 gagatccagaacgtgagatgtatgacgagggcccttaacacctgtcgtgtgcagacagac 493
QY 361 aaccacccaaagaccttaagggtccacctcattgtgcaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagaccttaagggtccacctcattgtgcaagtatctcccaaatgttagag 553
QY 421 attcttcagatatctccattaatgaaaggaaacaattagcctcaacctgcataagcaact 480
Db 554 attcttcagatatctccattaatgaaaggaaacaattagcctcaacctgcataagcaact 613
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Db 914 agactgattgaagaaagggtgtaaaagtgaaaaacagaccttcctctcaaaactc 973
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Db 1094 aacggcagctcgagagggcagcagctgctgtgctgtgctctcttctgtcttgcactg 1153
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RESULT 2

US-09-978-544A-522

; Sequence 522, Application US/09978544A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: KJlavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC13

; CURRENT APPLICATION NUMBER: US/09/978, 544A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db		134	atgaanaaccattccagccaanaatgcacaattctatctcttggcaattcttcagggtcg	193
QY		61	gtctctctgtctcttccaaaggagtgcacctgtagcagcggagatgcacactccccaaa	120
Db		194	gtctctctgtctcttccaaaggagtgcacctgtagcagcggagatgcacactccccaaa	253
QY		121	gctatgacacaactgtaacggtccggcaggggagagcgcccactcaggtgcactatggac	180
Db		254	gctatgacacaactgtaacggtccggcaggggagagcgcccactcaggtgcactatggac	313
QY		181	aaccggtgcaccccggttgcccttgctaaccgcagcaccatcctctatgtctyggaaatgac	240
Db		314	aaccggtgcaccccggttgcccttgctaaccgcagcaccatcctctatgtctyggaaatgac	373
QY		241	aagttggtgcctygatcctcgcgtgtgtccttctgagcaaacacccaaacgacacacgatc	300
Db		374	aagttggtgcctygatcctcgcgtgtgtccttctgagcaaacacccaaacgacacacgatc	433
QY		301	gagatccagaacgltggtatgttatgacgagggcccttacacctgtctcgtgtcagacagac	360
Db		434	gagatccagaacgltggtatgttatgacgagggcccttacacctgtctcgtgtcagacagac	493
QY		361	aaccaaccocaaagaacctctagagttccacctattgtgcaagatatccocaaattgtlagag	420
Db		494	aaccaaccocaaagaacctctagagttccacctattgtgcaagatatccocaaattgtlagag	553
QY		421	attcttcagatatctccatlaatlgaagggaacaataatagcctcacctgcatalgacaact	480
Db		554	attcttcagatatctccatlaatlgaagggaacaataatagcctcacctgcatalgacaact	613
QY		481	ggtagaocagagcctacggttaacttggagacacatctctccaaagcgttgtgcttgtg	540
Db		614	ggtagaocagagcctacggttaacttggagacacatctctccaaagcgttgtgcttgtg	673
QY		541	agtgaagaacgaataacttggnaattcagggcattcacoccggagcagtcaggggactacgag	600
Db		674	agtgaagaacgaataacttggnaattcagggcattcacoccggagcagtcaggggactacgag	733
QY		601	tgcagtgctcccaatgacgttgcccgccgccgtgtgtacggaagtaaagttcacccgtgaac	660
Db		734	tgcagtgctcccaatgacgttgcccgccgccgtgtgtacggaagtaaagttcacccgtgaac	793
QY		661	tatccaccatacatattcagaagccaagggtacacaggtgtcccccgttgggacaaaaggggaca	720
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Db		1034	ctgggcacacaccaaattgcagcatcatgtatttgyttccaggcgccgtcagcgaggtgagc	1093
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Db		1094	aacggacacgtcgaaggaggcagggtgctgtgtgctgtgctcttctgtgtcttgacactg	1153
QY		1021	cttctcaaaattt 1032	
Db		1154	cttctcaaaattt 1165	

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RESULT      3
US-09-978-681A-522
; Sequence 522, Application US/09978681A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC18
; CURRENT APPLICATION NUMBER: US/09/978,681A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 241 aagtgtgcttgatctctgcgtgtgtctctcttgagcaacaccccaacgcagtcagcacc 300
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RESULT 4

US-09-978-757A-522
 ; Sequence 522, Application US/09978757A

GENERAL INFORMATION:

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 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
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; PRIOR FILING DATE: 1998-05-15
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Best Local Similarity 100.0%; Pred. No. 6.3e-290;
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DB 194 gctgctctgtctcttccaaaggagtgcctgtgcgacggagatgccacttcccaaa 253

QY 121 gctatgacaacgtgacggtccggcaggaggagagcgccaccctcagttgcaatttgac 180
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QY 181 aaccgggtcaaccgggtgtgacctgtctaaaccgcagcaaccctctatgttggaaatgac 240
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DB 374 aagtgtgtccttgatctctcgctgtgtctcttgagcaacacccaaacagcagttacagcacc 433

QY 301 gagatccagaacgtgatgtgtatgacgagggtcccttacacctgtcgtgtgacagacgac 360
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QY 361 aaccaccaagacctaggtgccacctatgtgcaagtatctccaaaattgtagag 420
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RESULT 5

US-09-978-564A-522

; Sequence 522, Application US/09978564A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978, 564A
; CURRENT FILING DATE: 2001-10-16
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; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match      100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 atgaaaacatccagccaaaatgacaattctatctcttgggcaattcttcagggctg 60
Db      134 atgaaaacatccagccaaaatgacaattctatctcttgggcaattcttcagggctg 193

QY      61 gctgctctgtctctctccaaggagtgcccgctgcgcagcgagatgccaccttcccaaa 120
Db      194 gctgctctgtctctctccaaggagtgcccgctgcgcagcgagatgccaccttcccaaa 253

QY      121 gctatgacaacgtgacggtcccgccaggggagagcgccacccctcagtgcaattatgac 180
Db      254 gctatgacaacgtgacggtcccgccaggggagagcgccacccctcagtgcaattatgac 313

QY      181 aaccgggtcacccgggtgtgcctgtgctaaccgcagcaccaatcctctatgtctgggaatgac 240
Db      314 aaccgggtcacccgggtgtgcctgtgctaaccgcagcaccaatcctctatgtctgggaatgac 373

QY      241 aagtgtgtccttgatcctcgcgtgtgtcctcttgagcaacacccaaacgcagtlacagcattc 300
Db      374 aagtgtgtccttgatcctcgcgtgtgtcctcttgagcaacacccaaacgcagtlacagcattc 433

QY      301 gagatccagaacgtgatatgtatgacagagggcccttacacactgtcgttgcagacagac 360
Db      434 gagatccagaacgtgatatgtatgacagagggcccttacacactgtcgttgcagacagac 493

QY      361 aaccacccaagaacctctaggttccacctcatgtgtgcaagtatctcccaaatgttagag 420
Db      494 aaccacccaagaacctctaggttccacctcatgtgtgcaagtatctcccaaatgttagag 553

QY      421 attcttcagatatctccattaatgaaggaacaatatattagcctcacctgtacagaaact 480
Db      554 attcttcagatatctccattaatgaaggaacaatatattagcctcacctgtacagaaact 613

QY      481 ggtagaccagagcctaagtgtaacttggagacacacatctctccaaagcgttggcttgtg 540
Db      614 ggtagaccagagcctaagtgtaacttggagacacacatctctccaaagcgttggcttgtg 673
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QY 541 agtgaagacgaatacttggaaattcaaggcattcacccggagcagtcagggaactaacgag 600
|||||
Db 674 agtgaagacgaatacttggaaattcaaggcattcacccggagcagtcagggaactaacgag 733
QY 601 tgcagtgctccaatgacgtgcccgcgcgcgtgtgtaacgagtaaaaggtcacccgtgaac 660
|||||
Db 734 tgcagtgctccaatgacgtgcccgcgcgcgtgtgtaacgagtaaaaggtcacccgtgaac 793
QY 661 tatccaccatacatlctcagaagccaagggtacaggtgtcccccgttgaggacaaaaggggaca 720
|||||
Db 794 tatccaccatacatlctcagaagccaagggtacaggtgtcccccgttgaggacaaaaggggaca 853
QY 721 ctgcagtgatgaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 780
|||||
Db 854 ctgcagtgatgaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 913
QY 781 agactgattgaagaaagaagggtgaaagtggaaaacagacccttcctcctcaaaactc 840
|||||
Db 914 agactgattgaagaaagaagggtgaaagtggaaaacagacccttcctcctcaaaactc 973
QY 841 atcttctcaatgtctctgaacatgactatgggaactacacttgctggtccctccacaacag 900
|||||
Db 974 atcttctcaatgtctctgaacatgactatgggaactacacttgctggtccctccacaacag 1033
QY 901 ctgggccaacccaatgccaagcatgtctattgtgtccaggcgccgtcagcgaggtgagc 960
|||||
Db 1034 ctgggccaacccaatgccaagcatgtctattgtgtccaggcgccgtcagcgaggtgagc 1093
QY 961 aacggcacgtcggaggaggcgctgctgtgctgtcctctctgtcttgacactg 1020
|||||
Db 1094 aacggcacgtcggaggaggcgctgctgtgctgtcctctctgtcttgacactg 1153
QY 1021 ctctccaattt 1032
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Db 1154 ctctccaattt 1165

RESULT 6
US-09-999-831A-522
; Sequence 522, Application US/09999831A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C68
; CURRENT APPLICATION NUMBER: US/09/999,831A
; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-831A-522

Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaaatgacaaattctatctcttggcaattctcaagggtgctg 60
|||||
Db 134 atgaaaccatccagccaaaatgacaaattctatctcttggcaattctcaagggtgctg 193
QY 61 gctgctgtgtctcttccaaggagtgtcccggtgagcgagcgagatgccaacttcccaaa 120
|||||
Db 194 gctgctgtgtctcttccaaggagtgtcccggtgagcgagcgagatgccaacttcccaaa 253
QY 121 gctatgacaacgtgacgttccgagcgaggggagagcgccaccctcaggtgacattgac 180
|||||
Db 254 gctatgacaacgtgacgttccgagcgaggggagagcgccaccctcaggtgacattgac 313
QY 181 aaccggtgacccgggtgtgctgtgcttaaacgcagacacatcctctatgtctggagatgac 240
|||||
Db 314 aaccggtgacccgggtgtgctgtgcttaaacgcagacacatcctctatgtctggagatgac 373
QY 241 aagtggtgcctgatactcctgcgtgtgtctcttgaagcaaccccaaacgagtaacgacatc 300
|||||
Db 374 aagtggtgcctgatactcctgcgtgtgtctcttgaagcaaccccaaacgagtaacgacatc 433
QY 301 gagatccagaacgtgtgattgtatgacgagggcccttacacctgtcgtgtcagacagac 360
|||||
Db 434 gagatccagaacgtgtgattgtatgacgagggcccttacacctgtcgtgtcagacagac 493
QY 361 aaccacccaagaaccttagtggtccacctatgtgcaagtatctccaaaattgtagag 420
|||||
Db 494 aaccacccaagaaccttagtggtccacctatgtgcaagtatctccaaaattgtagag 553
QY 421 atttctcagatatctccattaatgaaagggaacaatatatagcctcaccgtgatacgaact 480
|||||
Db 554 atttctcagatatctccattaatgaaagggaacaatatatagcctcaccgtgatacgaact 613
QY 481 ggtagaaccagagcctacggttacttggagacacatctctccaaagcgtgtgtgttg 540
|||||
Db 614 ggtagaaccagagcctacggttacttggagacacatctctccaaagcgtgtgtgttg 673
QY 541 agtgaagacgaatacttggaaattcaaggcattcacccggagcagtcagggaactaacgag 600
|||||
Db 674 agtgaagacgaatacttggaaattcaaggcattcacccggagcagtcagggaactaacgag 733
QY 601 tgcagtgctccaatgacgtgcccgcgcgcgtgtgtaacgagtaaaaggtcacccgtgaac 660
|||||
Db 734 tgcagtgctccaatgacgtgcccgcgcgcgtgtgtaacgagtaaaaggtcacccgtgaac 793
QY 661 tatccaccatacatlctcagaagccaagggtacaggtgtcccccgttgaggacaaaaggggaca 720
|||||
Db 794 tatccaccatacatlctcagaagccaagggtacaggtgtcccccgttgaggacaaaaggggaca 853
QY 721 ctgcagtgatgaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 780
|||||
Db 854 ctgcagtgatgaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 913
QY 781 agactgattgaagaaagaagggtgaaagtggaaaacagacccttcctcctcaaaactc 840
|||||
Db 914 agactgattgaagaaagaagggtgaaagtggaaaacagacccttcctcctcaaaactc 973
QY 841 atcttctcaatgtctctgaacatgactatgggaactacacttgctggtccctccacaacag 900
|||||
Db 974 atcttctcaatgtctctgaacatgactatgggaactacacttgctggtccctccacaacag 1033

QY	901	ctgggccaacacaatgccaagcatcatgtctatttggccaagcgccgtccaagcaggtgagc	960
Db	1034	ctgggccaacacaatgccaagcatcatgtctatttggccaagcgccgtccaagcaggtgagc	1093
QY	961	aacggcacgtcgaggaaggcaggctgcctctgctgcctctctgtgtcttgcaactg	1020
Db	1094	aacggcacgtcgaggaaggcaggctgcctctgctgcctctctgtgtcttgcaactg	1153
QY	1021	ctctctcaaatctt	1032
Db	1154	ctctctcaaatctt	1165

RESULT 7
US-09-999-829A-522
; Sequence 522, Application US/09999829A

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/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C61
/ CURRENT APPLICATION NUMBER: US/09/999,829A
/ CURRENT FILING DATE: 2002-03-19
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 522
/ LENGTH: 1679
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-999-829A-522

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Query Match	100.0%;	Score 1032;	DB 5;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 6.3e-290;		
Matches 1032; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 atgaaaccatccagccaaaaatgccaattctatctcttggccaattccaagggtg 60
|||||
Db 134 atgaaaccatccagccaaaaatgccaattctatctcttggccaattccaagggtg 193
QY 61 gctgctctgtgtctcttccaaggagtgtccctgtgcgcagcgagatgccaccttcccaaa 120
|||||
Db 194 gctgctctgtgtctcttccaaggagtgtccctgtgcgcagcgagatgccaccttcccaaa 253
QY 121 gctatggacaacgtgacggtccggcgaggggagagcgccaacctcagtgtaattaac 180
|||||
Db 254 gctatggacaacgtgacggtccggcgaggggagagcgccaacctcagtgtaattaac 313

QY	181	aaccggygtacaccgggtgtgcctcgtgtacaaaccgcagcacacatccttatgtctyggatgac	240
Db	314	aaccggygtacaccgggtgtgcctcgtgtacaaaccgcagcacacatccttatgtctyggatgac	373
QY	241	aagtggtgtcctgtatcctcgcgtgtgtctctctgtagcaacacccaaacgcagttacagatc	300
Db	374	aagtggtgtcctgtatcctcgcgtgtgtctctctgtagcaacacccaaacgcagttacagatc	433
QY	301	gagatccagaacgctgtgatgtgtatgtacgagagggcccttacacctgtctgtgtcagacagac	360
Db	434	gagatccagaacgctgtgatgtgtatgtacgagagggcccttacacctgtctgtgtcagacagac	493
QY	361	aaccaccccaaaagacctctagagttccacctatgtgtcaagttatctccaaaattgtatgag	420
Db	494	aaccaccccaaaagacctctagagttccacctatgtgtcaagttatctccaaaattgtatgag	553
QY	421	attcttcagatatctccatnaatgaagggaaacaatatatagcctcacctcagtaagcaact	480
Db	554	attcttcagatatctccatnaatgaagggaaacaatatatagcctcacctcagtaagcaact	613
QY	481	ggtagaccagagcgtacggttaactgtgagagacacatctctccaaagcggttggttggtg	540
Db	614	ggtagaccagagcgtacggttaactgtgagagacacatctctccaaagcggttggttggtg	673
QY	541	agtgaaagacgaatacttggaattcagggcatcacccgggagcagttcaggggactacgag	600
Db	674	agtgaaagacgaatacttggaattcagggcatcacccgggagcagttcaggggactacgag	733
QY	601	tgcattgctctccaatgacggtgcccgcgcctgtgtacgagaggtaaagttcacccgtgaac	660
Db	734	tgcattgctctccaatgacggtgcccgcgcctgtgtgtacgagaggtaaagttcacccgtgaac	793
QY	661	tatcacccatacatcttcagaagccaaggtacaggtgtccccgttgggacaaaaggggaca	720
Db	794	tatcacccatacatcttcagaagccaaggtacaggtgtccccgttgggacaaaaggggaca	853
QY	721	ctgcagttgtgaagcctcagcagtcacctcagcagaaatccagttgtgtacaagatgacaaa	780
Db	854	ctgcagttgtgaagcctcagcagtcacctcagcagaaatccagttgtgtacaagatgacaaa	913
QY	781	agac.tgatgtgaaggaagaaggggtgaagttgnaaacagaccttctctcaaaatc	840
Db	914	agac.tgatgtgaaggaagaaggggtgaagttgnaaacagaccttctctcaaaatc	973
QY	841	atctcttcaatgtctctgtgaacaatgactatggyaactacacacttgctgtgacctccaacag	900
Db	974	atctcttcaatgtctctgtgaacaatgactatggyaactacacacttgctgtgacctccaacag	1033
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Db	1034	ctgsgccacacccaatgtgccagcatcatgtatttggccagggcgccgtcaagcgaggtgagc	1093
QY	961	aacggaacgtcgaggaagggcaggtctgtctgtgtctgtgtcctcttctgtgtcttgcaactg	1020
Db	1094	aacggaacgtcgaggaagggcaggtctgtctgtgtgtctgtgtcctcttctgtgtcttgcaactg	1153
QY	1021	cttctcaaatctt 1032	
Db	1154	cttctcaaatctt 1165	

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; RESULT      8
; US-09-978-375A-522
; Sequence 522, Application US/09978375A
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi
;   APPLICANT: Baker Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan
;   APPLICANT: Ferrara, Napoleon
;   APPLICANT: Filvaroff, Ellen

```

```

; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC24
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-375A-522

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Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgaaaccatccagccaaaatgacaaattctatctcttgaggcaatctccagggtg 60
Db 134 atgaaaccatccagccaaaatgacaaattctatctcttgaggcaatctccagggtg 193
QY 61 gctgctgtgtctcttccaaaggagtcgccgtgcgcagcgagatgccaacttcccaaa 120
Db 194 gctgctgtgtctcttccaaaggagtcgccgtgcgcagcgagatgccaacttcccaaa 253
QY 121 gctatgacaacgtgacgtccgcaggggagagcgccaccctcaggtgacattgac 180
Db 254 gctatgacaacgtgacgtccgcaggggagagcgccaccctcaggtgacattgac 313
QY 181 aaccgggtaccccggtggtgctgctaaaccgcagccaccatcctctatgtggaatgac 240
Db 314 aaccgggtaccccggtggtgctgctaaaccgcagccaccatcctctatgtggaatgac 373
QY 241 aagtgtgctgtgattcctcgtgctgtgtctcttgagcaacaccccaacgcagtaacgcatc 300
Db 374 aagtgtgctgtgattcctcgtgctgtgtctcttgagcaacaccccaacgcagtaacgcatc 433
QY 301 gagatccagaacgtgattgtatgacgaaggcccttacacctgtcgtgacagacagac 360
Db 434 gagatccagaacgtgattgtatgacgaaggcccttacacctgtcgtgacagacagac 493
QY 361 aaccaccccaagaaccttaggtgtccacctcatgtgcaagtatctcccaaaatgtagag 420
Db 494 aaccaccccaagaaccttaggtgtccacctcatgtgcaagtatctcccaaaatgtagag 553
QY 421 attcttcagatatctccattaatgaagggaacaataatagacctcactgcatagcaact 480
Db 554 attcttcagatatctccattaatgaagggaacaataatagacctcactgcatagcaact 613
QY 481 gtagaccagagcctacggttacttgtagaacacatctctcccaaaagcgttgctttgtg 540
Db 614 gtagaccagagcctacggttacttgtagaacacatctctcccaaaagcgttgctttgtg 673

```

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QY 541 agtgaagcagaacttggaaattcagggtcatcccggtgagcagtcagggtactagag 600
Db 674 agtgaagcagaacttggaaattcagggtcatcccggtgagcagtcagggtactagag 733
QY 601 tgcagtgctctccaatgacgtgtgcccgcgccctgtgtacggagagtaaaagtcaccgtgaac 660
Db 734 tgcagtgctctccaatgacgtgtgcccgcgccctgtgtacggagagtaaaagtcaccgtgaac 793
QY 661 tatccaccatacatcttcagaagccaagggttaaggtgtccccgttggacaaaagggtgaca 720
Db 794 tatccaccatacatcttcagaagccaagggttaaggtgtccccgttggacaaaagggtgaca 853
QY 721 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacaagatgacaaa 780
Db 854 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacaagatgacaaa 913
QY 781 agactgattgaagaaagaagggtgaaggtggaaaacagaccttctctcaaaactc 840
Db 914 agactgattgaagaaagaagggtgaaggtggaaaacagaccttctctcaaaactc 973
QY 841 atctcttcaatgtctcttgaaacatgactatggtggaactacacttgcgtggtccccaacag 900
Db 974 atctcttcaatgtctcttgaaacatgactatggtggaactacacttgcgtggtccccaacag 1033
QY 901 ctgggccacacccaatgcccagcatcatgtctattggtccaggccgctcagcgagtgagc 960
Db 1034 ctgggccacacccaatgcccagcatcatgtctattggtccaggccgctcagcgagtgagc 1093
QY 961 aacggcacgtcgaggaaggcgagcgtgctgtgctgtgcctcttctgtcttgacactg 1020
Db 1094 aacggcacgtcgaggaaggcgagcgtgctgtgctgtgcctcttctgtcttgacactg 1153
QY 1021 ctctcaaatlt 1032
Db 1154 ctctcaaatlt 1165

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RESULT 9
US-09-978-423A-522
; Sequence 522, Application US/09978423A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC21
; CURRENT APPLICATION NUMBER: US/09/978,423A

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Fri Jul 12 08:37:52 2002

us-09-700-397-1.rnp

Page 14

1	CURRENT FILING DATE:	2002-05-16
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3	PRIOR FILING DATE:	2001-07-30
4	PRIOR APPLICATION NUMBER:	60/062250
5	PRIOR FILING DATE:	1997-10-17
6	PRIOR APPLICATION NUMBER:	60/064249
7	PRIOR FILING DATE:	1997-11-03
8	PRIOR APPLICATION NUMBER:	60/065311
9	PRIOR FILING DATE:	1997-11-13
10	PRIOR APPLICATION NUMBER:	60/066364
11	PRIOR FILING DATE:	1997-11-21
12	PRIOR APPLICATION NUMBER:	60/077450
13	PRIOR FILING DATE:	1998-03-10
14	PRIOR APPLICATION NUMBER:	60/077632
15	PRIOR FILING DATE:	1998-03-11
16	PRIOR APPLICATION NUMBER:	60/077641
17	PRIOR FILING DATE:	1998-03-11
18	PRIOR APPLICATION NUMBER:	60/077649
19	PRIOR FILING DATE:	1998-03-11
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21	PRIOR FILING DATE:	1998-03-12
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23	PRIOR FILING DATE:	1998-03-13
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42	PRIOR APPLICATION NUMBER:	60/079728
43	PRIOR FILING DATE:	1998-03-27
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50	PRIOR APPLICATION NUMBER:	60/080105
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53	PRIOR FILING DATE:	1998-03-31
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55	PRIOR FILING DATE:	1998-03-31
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73	PRIOR FILING DATE:	1998-04-08

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6	PRIOR FILING DATE: 1998-04-15
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21	PRIOR APPLICATION NUMBER: 60/082704
22	PRIOR FILING DATE: 1998-04-22
23	PRIOR APPLICATION NUMBER: 60/082804
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33	PRIOR APPLICATION NUMBER: 60/083322
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35	PRIOR APPLICATION NUMBER: 60/083392
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 5; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaaaatgcacaattctatctcttgggcaattctcaaggcgctg 60
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QY 61 gctgctgtgtctctctccaaaggagtgcccgctgacgagcgagatgcaaccttcccaaa 120
Db 194 gctgctgtgtctctctccaaaggagtgcccgctgacgagcgagatgcaaccttcccaaa 253
QY 121 gctatgacaacgtgacggtccggcagggggagagcgccacctgaagtgacataatgac 180
Db 254 gctatgacaacgtgacggtccggcagggggagagcgccacctgaagtgacataatgac 313
QY 181 aaccgggtcacccgggtgctgctgtcaaacccgacacccatcctctatgctgggaatgac 240
Db 314 aaccgggtcacccgggtgctgctgtcaaacccgacacccatcctctatgctgggaatgac 373
QY 241 aagtgtgctgtagctcctcgctgtgtctctcttgagcaacacccaaacgagtaacgacatc 300
Db 374 aagtgtgctgtagctcctcgctgtgtctctcttgagcaacacccaaacgagtaacgacatc 433
QY 301 gagatccagaacgtgtagtgtatgacgaaggcccttaacacctgctcggtgacagacac 360
Db 434 gagatccagaacgtgtagtgtatgacgaaggcccttaacacctgctcggtgacagacac 493
QY 361 aaccacccaaagaccttaggggtccacctcatltgtgaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagaccttaggggtccacctcatltgtgaagtatctcccaaatgttagag 553
QY 421 attcttcagatatctccattaatgaagggaacaatatattagcctcaactgc tagcaact 480
Db 554 attcttcagatatctccattaatgaagggaacaatatattagcctcaactgc tagcaact 613
QY 481 ggtagaccagaagcctacggttacttgaagacacatctctccaaagcggttgctttgtg 540
Db 614 ggtagaccagaagcctacggttacttgaagacacatctctccaaagcggttgctttgtg 673
QY 541 agtgaagacgaatacttgaataattcaaggacatcaaccgggagcagtcagggaactacgag 600
Db 674 agtgaagacgaatacttgaataattcaaggacatcaaccgggagcagtcagggaactacgag 733
QY 601 tgcagtgctccaatgacgtgycgcgcgcctgtgtacgagagagtaaggtcacacgtgaac 660
Db 734 tgcagtgctccaatgacgtgycgcgcgcctgtgtacgagagagtaaggtcacacgtgaac 793
QY 661 tatccaccatacatltcagaagccaagggtacaggtgtcccggtggacaanaaggggaca 720
Db 794 tatccaccatacatltcagaagccaagggtacaggtgtcccggtggacaanaaggggaca 853

QY 721 ctgcagtgtaagcctcagcagctccctcagcagaattcccaagtggtacaagatgacaaa 780
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QY 781 agactgattgaaggaagaaggggtgaagtgaanaacagaccttctcctcaaacctc 840
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QY 841 atcttctcaatgtctctgaacacagactatgggaactacacttgcgtgctctcaacaag 900
Db 974 atcttctcaatgtctctgaacacagactatgggaactacacttgcgtgctctcaacaag 1033
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Db 1034 ctgggccacacccaattccagcactatgtctatttggtcgaagcgccgtcagcaggtgagc 1093
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Db 1094 aacggcacgtcgaagaggcgacgctgctgtgctgctgctcctctctgtctgcaacctg 1153
QY 1021 ctctcaaat 1032
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RESULT 10
US-10-013-921A-522
; Sequence 522, Application US/10013921A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C84
; CURRENT APPLICATION NUMBER: US/10/013, 921A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1997-11-21
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5	PRIOR FILING DATE: 1998-03-11
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3	PRIOR APPLICATION NUMBER: 60/082568
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16	PRIOR FILING DATE: 1998-04-22
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18	PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gctgctctgtctctccaaagagtgcccgagcgagatggccacctcccaaa 120
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Db 194 gctgctctgtctctccaaagagtgcccgagcgagatggccacctcccaaa 253

QY 121 gctatgacaacgtgacggtccggcaggggagagcgccacctcagtgcaattgac 180
    |||||||
Db 254 gctatgacaacgtgacggtccggcaggggagagcgccacctcagtgcaattgac 313

QY 181 aaccgggtcacccgggtggccttgcttaaacccgacacccatccttatgtgtggaatgac 240
    |||||||
Db 314 aaccgggtcacccgggtggccttgcttaaacccgacacccatccttatgtgtggaatgac 373

QY 241 aagtggtgctgatacctcgctgtgctctctgagcaaacacccaaacgagtaagcattc 300
    |||||||
Db 374 aagtggtgctgatacctcgctgtgctctctgagcaaacacccaaacgagtaagcattc 433

QY 301 gagatccagaacgtgagtgatgtatgacagaggcccttaacacctgtcgtgacagacagac 360
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Db 434 gagatccagaacgtgagtgatgtatgacagaggcccttaacacctgtcgtgacagacagac 493

QY 361 aaccacccaaagacctctaggtgtccacctattgtgcaagtatatctccaaatgtagag 420
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Db 494 aaccacccaaagacctctaggtgtccacctattgtgcaagtatatctccaaatgtagag 553

QY 421 attcttcagatatctccaatatgaaagggaacaatatagacctcagtcagtaagcaact 480
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Db 554 attcttcagatatctccaatatgaaagggaacaatatagacctcagtcagtaagcaact 613

QY 481 ggtagaccagagcctacggttacttgtagagacacatctctccaaacggttgctttgtg 540
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QY 541 agtgaagacgaatacttggaattccagggcatacccgaggagcagtcagggtactacgag 600
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QY 721 ctgcagtgtagagcctcagcaggtcccccacagcaattccagtggtacaaagatgacaaa 780
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Db 914 agactgattgaagaaagggtgtgaagtgtgaaaaacagaccttctcacaactc 973

QY 841 atcttcttcaatgtctctaaacatgacatggaactaaccttggtggcctccacaag 900
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QY 1021 ctctcacaattt 1032
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Db 1154 ctctcacaattt 1165
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RESULT 11
US-10-013-929A-522
; Sequence 522, Application US/10013929A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C89
; CURRENT APPLICATION NUMBER: US/10/013, 929A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
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70	PRIOR FILING DATE: 1998-05-15

Query Match	100.0%;	Score 1032;	DB 6;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 6.3e-290;		

Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	194	gctgctctgtctcttccaagagtgccgtgcagcgagatgccacttcccaaa	253
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RESULT 12
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C77
; CURRENT APPLICATION NUMBER: US/10/013,918A
; PRIOR FILING DATE: 2002-03-25
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; PRIOR FILING DATE: 1998-05-15

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Db      194 gctgctctgtctcttccaagagtgcccgctgcgacgagagatgccacttcccca 253

QY      121 gctatgacaacgtgacggtccgcgaggggagagcgccaccctcaagtgtaactattgac 180
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Db 254 gctatggacaacgtgaacggtccggcagggggagagcgccaccctcaggtgtgcaactattgac 313
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Db 314 aaccgggtcaccggggtggtcgtgttaaacccgcaaccatcctctatgttggaaatgac 373
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Db 374 aagtgtgctgtgatcctcgtgtgttctctctgtgcaacacccaacgcaatgacacac 433
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QY 661 tatccaccatacatcttcaggaaaggggtacaggtgtcccggtggagcaaaaaggggaca 720
Db 794 tatccaccatacatcttcaggaaaggggtacaggtgtcccggtggagcaaaaaggggaca 853
QY 721 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtgtacaagatgacaaa 780
Db 854 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtgtacaagatgacaaa 913
QY 781 agactgatlgaaagaaagggtgaagtgtaaaagtgtgaaaaacagaccttctctcaaaactc 840
Db 914 agactgatlgaaagaaagggtgaagtgtaaaagtgtgaaaaacagaccttctctcaaaactc 973
QY 841 atcttctcaatgtctctgaacatgacatgtggaactacactgtgctggcctccaacaag 900
Db 974 atcttctcaatgtctctgaacatgacatgtggaactacactgtgctggcctccaacaag 1033
QY 901 ctgggccacaccaatgtccagcatcatgtatttgtgccagggcgctcagcgaggtgagc 960
Db 1034 ctgggccacaccaatgtccagcatcatgtatttgtgccagggcgctcagcgaggtgagc 1093
QY 961 aacggcagctcgaggagggcaggtcgtctgtgtcctctctgtgtcttgacacctg 1020
Db 1094 aacggcagctcgaggagggcaggtcgtctgtgtcctctctgtgtcttgacacctg 1153
QY 1021 ctctccaattt 1032
Db 1154 ctctccaattt 1165

RESULT 13
US-10-017-082A-522

; Sequence 522, Application US/10017082A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C71
; CURRENT APPLICATION NUMBER: US/10/017,082A
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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; PRIOR APPLICATION NUMBER: 60/079664
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; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923

; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 60/080105
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080107
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 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
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 ; PRIOR FILING DATE: 1998-04-08
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 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
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 ; PRIOR FILING DATE: 1998-04-09
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 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082700
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
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 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
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 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083500
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083742
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
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 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
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 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 6.3e-290;
 Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaacatccagccaaatgcaaatctctcttgggcaatcttcaagggctg 60
 Db 134 atgaaacatccagccaaatgcaaatctctcttgggcaatcttcaagggctg 193
 QY 61 gctgctctgtgtctcttccaagagtgcccggtgcgacggagatgccaacttcccaaa 120
 Db 194 gctgctctgtgtctcttccaagagtgcccggtgcgacggagatgccaacttcccaaa 253
 QY 121 gctatgcaacgtgacggtccgcaaggagagcgccaccctcagtgcaattatgac 180
 Db 254 gctatgcaacgtgacggtccgcaaggagagcgccaccctcagtgcaattatgac 313
 QY 181 aaccggtcaccgggtggtcgtgctaaccgcagcaccatccttatgtggaatgac 240
 Db 314 aaccggtcaccgggtggtcgtgctaaccgcagcaccatccttatgtggaatgac 373
 QY 241 aagtgtgcttgatcctcgtggtgtctcttgagcaacccaacgagttacagatc 300
 Db 374 aagtgtgcttgatcctcgtggtgtctcttgagcaacccaacgagttacagatc 433
 QY 301 gagatccagaacgtgatgtgtatgacgagggcccttacacctgtctgtgcagaaagac 360

Db 434 gagatccagaacgtgtagtgtatgacgagggcccttacacctgctcggtgcagacagac 493
QY 361 aaccacccaaagacctctaggggtccacctcatgtgtcaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagacctctaggggtccacctcatgtgtcaagtatctcccaaatgttagag 553
QY 421 attcttcagatatctccattaatgaagggaacaaatattagcctcacctgcataagcaact 480
Db 554 attcttcagatatctccattaatgaagggaacaaatattagcctcacctgcataagcaact 613
QY 481 gtagaccagagcctaaggttactgtgagacacatctctccaaagcgtgtgtgtgtg 540
Db 614 gtagaccagagcctaaggttactgtgagacacatctctccaaagcgtgtgtgtgtg 673
QY 541 agtgaagacgaatacttgyaaattcagggcataccccgggagcagtcaggggactagag 600
Db 674 agtgaagacgaatacttgyaaattcagggcataccccgggagcagtcaggggactagag 733
QY 601 tgcagtgccctccaatgacgtgcccgcgccgtgtgtacggaagtaaaaggtcacccgtgac 660
Db 734 tgcagtgccctccaatgacgtgcccgcgccgtgtgtacggaagtaaaaggtcacccgtgac 793
QY 661 tatccaccatacattcagaagaagccaaaggtacacagtggtccccgttggacaaaggggaca 720
Db 794 tatccaccatacattcagaagaagccaaaggtacacagtggtccccgttggacaaaggggaca 853
QY 721 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 780
Db 854 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 913
QY 781 agactgattgaaggaagaaggggtgaagtggaacacagaccttctcctcaaacctc 840
Db 914 agactgattgaaggaagaaggggtgaagtggaacacagaccttctcctcaaacctc 973
QY 841 atcttctcaatgtctctgaaacatgactatgggaactacacctgctgtgcccctcaacaag 900
Db 974 atcttctcaatgtctctgaaacatgactatgggaactacacctgctgtgcccctcaacaag 1033
QY 901 ctgggccacacccaatgccaagcatatgtattgtgtccaggcgcgtcagcgaggtgagc 960
Db 1034 ctgggccacacccaatgccaagcatatgtattgtgtccaggcgcgtcagcgaggtgagc 1093
QY 961 aacgycacgctcgaaggaaggcagcgtcgctcgtgctgcttctctgtgtctgacactg 1020
Db 1094 aacgycacgctcgaaggaaggcagcgtcgctcgtgctgcttctctgtgtctgacactg 1153
QY 1021 ctctcacaattt 1032
Db 1154 ctctcacaattt 1165
RESULT 14
US-10-119-480-125
; Sequence 125, Application us/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 125

; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-125
Query Match 100.0%; Score 1032; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgaaacacatccagccaaaatgacaaattctatctcttgggaactcttcacggggctg 60
Db 134 atgaaacacatccagccaaaatgacaaattctatctcttgggaactcttcacggggctg 193
QY 61 gctgctctgtgtctcttccaaggagtgcccggtgcgcagcgagatgccaacttcccaaaa 120
Db 194 gctgctctgtgtctcttccaaggagtgcccggtgcgcagcgagatgccaacttcccaaaa 253
QY 121 gctatggacaacgtgacggtcccggaaggggagagcgccaccctcaggtgcaactattgac 180
Db 254 gctatggacaacgtgacggtcccggaaggggagagcgccaccctcaggtgcaactattgac 313
QY 181 aaccgggtcaccccggtgtgacctgttaaacccgacgaaccatcttatgtctgggaatgac 240
Db 314 aaccgggtcaccccggtgtgacctgttaaacccgacgaaccatcttatgtctgggaatgac 373
QY 241 aagtggtgcttgatcctcgcgtgtgtccttctgagcaaaccccaaacgcagttacagcaltc 300
Db 374 aagtggtgcttgatcctcgcgtgtgtccttctgagcaaaccccaaacgcagttacagcaltc 433
QY 301 gagatccagaacgtgtagtgtatgacgagggcccttacacctgctcggtgcagacagac 360
Db 434 gagatccagaacgtgtagtgtatgacgagggcccttacacctgctcggtgcagacagac 493
QY 361 aaccacccaaagacctctaggggtccacctcatgtgtcaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagacctctaggggtccacctcatgtgtcaagtatctcccaaatgttagag 553
QY 421 attcttcagatatctccattaatgaagggaacaaatattagcctcacctgcataagcaact 480
Db 554 attcttcagatatctccattaatgaagggaacaaatattagcctcacctgcataagcaact 613
QY 481 gtagaccagagcctaaggttactgtgagacacatctctccaaagcgtgtgtgtgtg 540
Db 614 gtagaccagagcctaaggttactgtgagacacatctctccaaagcgtgtgtgtgtg 673
QY 541 agtgaagacgaatacttgyaaattcagggcataccccgggagcagtcaggggactagag 600
Db 674 agtgaagacgaatacttgyaaattcagggcataccccgggagcagtcaggggactagag 733
QY 601 tgcagtgccctccaatgacgtgcccgcgccgtgtgtacggaagtaaaaggtcacccgtgac 660
Db 734 tgcagtgccctccaatgacgtgcccgcgccgtgtgtacggaagtaaaaggtcacccgtgac 793
QY 661 tatccaccatacattcagaagaagccaaaggtacacagtggtccccgttggacaaaggggaca 720
Db 794 tatccaccatacattcagaagaagccaaaggtacacagtggtccccgttggacaaaggggaca 853
QY 721 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 780
Db 854 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtggtacaaagatgacaaa 913
QY 781 agactgattgaaggaagaaggggtgaagtggaacacagaccttctcctcaaacctc 840
Db 914 agactgattgaaggaagaaggggtgaagtggaacacagaccttctcctcaaacctc 973
QY 841 atcttctcaatgtctctgaaacatgactatgggaactacacctgctgtgcccctcaacaag 900
Db 974 atcttctcaatgtctctgaaacatgactatgggaactacacctgctgtgcccctcaacaag 1033
QY 901 ctgggccacacccaatgccaagcatatgtattgtgtccaggcgcgtcagcgaggtgagc 960
Db 1034 ctgggccacacccaatgccaagcatatgtattgtgtccaggcgcgtcagcgaggtgagc 1093

QY 961 aacggcacgtcagaggagggcaggtcgctgctgtgctctctctgtgctcttgacactg 1020
|||
Db 1094 aacggcacgtcagaggagggcaggtcgctgctgtgctgctctctctgtgctcttgacactg 1153
QY 1021 ctctcaattt 1032
|||
Db 1154 ctctcaattt 1165

RESULT 15
US-10-121-049-375

; Sequence 375, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 375
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-375

Query Match 100.0%; Score 1032; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaatgacaaattctatctcttgggaatcttcaagggctg 60
|||
Db 134 atgaaaccatccagccaaatgacaaattctatctcttgggaatcttcaagggctg 193
QY 61 gctgctctgtgtctcttccaagagtgcccgctgagcgagatgccaacttcccaaa 120
|||
Db 194 gctgctctgtgtctcttccaagagtgcccgctgagcgagatgccaacttcccaaa 253
QY 121 gctatggacaacgtgaacggtccggcaggggagagcgccaccctcaggtgcaatttgac 180
|||
Db 254 gctatggacaacgtgaacggtccggcaggggagagcgccaccctcaggtgcaatttgac 313
QY 181 aaccgggtcacccgggtggtgctgtaaacccgagcaccatcttatgtctgggaatgac 240
|||
Db 314 aaccgggtcacccgggtggtgctgtaaacccgagcaccatcttatgtctgggaatgac 373
QY 241 aagtgtgctgctgacccctcgctgtgctctcttgaagcaaacccaaacagcagtacagc 300
|||
Db 374 aagtgtgctgctgacccctcgctgtgctctcttgaagcaaacccaaacagcagtacagc 433
QY 301 gagatccagaacgtgagatgtgtatgacagagggcccttacacctgtctggtgacagac 360
|||
Db 434 gagatccagaacgtgagatgtgtatgacagagggcccttacacctgtctggtgacagac 493

QY 361 aaccaccaagacctgaagggtccacctcatgtgtgaagtatctccaaatgtagag 420
|||
Db 494 aaccaccaagacctgaagggtccacctcatgtgtgaagtatctccaaatgtagag 553
QY 421 attcttcaatatctccaattaatgaagggaacaatatattagcctcaactgtacagcaact 480
|||
Db 554 attcttcaatatctccaattaatgaagggaacaatatattagcctcaactgtacagcaact 613
QY 481 ggtagaccagagcctacaggttacttgaagacacatctctccaaagcgttgcttgtg 540
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Db 614 ggtagaccagagcctacaggttacttgaagacacatctctccaaagcgttgcttgtg 673
QY 541 agtgaagacgaatacttgaatattcaggagcatcacccgggagcaggtcagggtacagag 600
|||
Db 674 agtgaagacgaatacttgaatattcaggagcatcacccgggagcaggtcagggtacagag 733
QY 601 tgcagtgcctccaatgaacgtgcccgcgctgtgtacggagagtaaaagttcacccgtgaac 660
|||
Db 734 tgcagtgcctccaatgaacgtgcccgcgctgtgtacggagagtaaaagttcacccgtgaac 793
QY 661 tatccaccatacatttcagaagcccaagggtacaggtgtcccccgttgagcaaaaaggagaca 720
|||
Db 794 tatccaccatacatttcagaagcccaagggtacaggtgtcccccgttgagcaaaaaggagaca 853
QY 721 ctgcagtggtgaagcctcagcagctcccccacagcagaattccacgtgtgtacaagatgacaa 780
|||
Db 854 ctgcagtggtgaagcctcagcagctcccccacagcagaattccacgtgtgtacaagatgacaa 913
QY 781 agactgattgaaggaaagaaagggtgtgaagttggaaaacagacccttccctcctcaaaactc 840
|||
Db 914 agactgattgaaggaaagaaagggtgtgaagttggaaaacagacccttccctcctcaaaactc 973
QY 841 atcttctcaatgtctctgaacatgaactatggaactacacttgcgtggtcctccaaag 900
|||
Db 974 atcttctcaatgtctctgaacatgaactatggaactacacttgcgtggtcctccaaag 1033
QY 901 ctgggccaacccaatgccagcatcatgtatttggccaaggcgccgtcagcgagtgagc 960
|||
Db 1034 ctgggccaacccaatgccagcatcatgtatttggccaaggcgccgtcagcgagtgagc 1093
QY 961 aacggcacgtcagaggagggcaggtcgctgctgtgctgctctctctgtcttgacactg 1020
|||
Db 1094 aacggcacgtcagaggagggcaggtcgctgctgtgctgctctctctgtcttgacactg 1153
QY 1021 ctctcaattt 1032
|||
Db 1154 ctctcaattt 1165

Search completed: July 12, 2002, 00:32:21
Job time: 11044 sec

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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 20:38:02 ; Search time 5033.46 Seconds
(without alignments)
4435.759 Million cell updates/sec

Title: US-09-700-397-1
Perfect score: 1032
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 segs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. NO. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	1032	100.0	1032	28	US-09-700-397-1	Sequence 1, Appl1
2	1032	100.0	1333	60	US-60-213-360-4483	Sequence 4483, Ap
3	1032	100.0	1679	17	US-09-380-138-522	Sequence 522, App
4	1032	100.0	1679	34	US-09-918-585A-522	Sequence 522, App
5	1032	100.0	1679	36	US-09-978-188A-522	Sequence 522, App
6	1032	100.0	1679	36	US-09-978-189-522	Sequence 522, App
7	1032	100.0	1679	36	US-09-978-191A-522	Sequence 522, App
8	1032	100.0	1679	36	US-09-978-192-522	Sequence 522, App
9	1032	100.0	1679	36	US-09-978-192A-522	Sequence 522, App
10	1032	100.0	1679	36	US-09-978-193A-522	Sequence 522, App
11	1032	100.0	1679	36	US-09-978-194A-522	Sequence 522, App
12	1032	100.0	1679	36	US-09-978-295A-522	Sequence 522, App
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14	1032	100.0	1679	36	US-09-978-299A-522	Sequence 522, App
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16	1032	100.0	1679	36	US-09-978-585A-522	Sequence 522, App
17	1032	100.0	1679	36	US-09-978-608-522	Sequence 522, App
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19	1032	100.0	1679	36	US-09-978-643-522	Sequence 522, App
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21	1032	100.0	1679	36	US-09-978-665A-522	Sequence 522, App
22	1032	100.0	1679	36	US-09-978-697-522	Sequence 522, App
23	1032	100.0	1679	36	US-09-978-802A-522	Sequence 522, App
24	1032	100.0	1679	36	US-09-978-824-522	Sequence 522, App
25	1032	100.0	1679	36	US-09-981-915A-522	Sequence 522, App
26	1032	100.0	1679	36	US-09-999-830A-522	Sequence 522, App
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28	1032	100.0	1679	36	US-09-999-833A-522	Sequence 522, App
29	1032	100.0	1679	36	US-09-999-834A-522	Sequence 522, App
30	1032	100.0	1679	37	US-10-002-796-103	Sequence 103, App
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34	1032	100.0	1679	37	US-10-020-445A-522	Sequence 522, App
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36	1032	100.0	1679	37	US-10-066-198-103	Sequence 103, App
37	1032	100.0	1679	37	US-10-066-198-103	Sequence 103, App
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39	1032	100.0	1679	37	US-10-066-211-103	Sequence 103, App
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45	1032	100.0	1693	28	US-09-700-397-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT
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US-09-700-397-1
; Sequence 1, Application US/09700397
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Novel Polypeptides, cDNA encoding the same, and use of them
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1

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Query Match 100.0%; Score 1032; DB 28; Length 1032;
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RESULT 2
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; Sequence 4483, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Us
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide P
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 4483
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 228470.1
; NAME/KEY: unsure
; LOCATION: 120, 124, 169, 173
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-360-4483

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Query Match 100.0%; Score 1032; DB 60; Length 1333;
Best Local Similarity 100.0%; Pred. No. 8.5e-288;
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RESULT 3
US-09-380-138-522
; Sequence 522, Application US/09380138
; GENERAL INFORMATION:
; APPLICANT: Wood, William I.
; APPLICANT: Goddard, Audrey
; APPLICANT: Garney, Austin
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2630R1E
; CURRENT APPLICATION NUMBER: US/09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: US 60/084,639
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; PRIOR APPLICATION NUMBER: US 60/084,637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: US 60/084,643
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: US 60/084,598
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; PRIOR APPLICATION NUMBER: US 60/085,697
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; PRIOR APPLICATION NUMBER: US 60/085,580
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; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/085,700
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; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/086,486
; PRIOR FILING DATE: 1998-05-22
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; PRIOR APPLICATION NUMBER: US 60/086,430
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/087,106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,038
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 538
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-380-138-522
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Query Match 100.0%; Score 1032; DB 17; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgaaaacatccagccaaaatgacaaattctatctcttggcgaattcaccgagctg 60
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Db 134 atgaaaacatccagccaaaatgacaaattctatctcttggcgaattcaccgagctg 193

QY 61 gctgctctgtctcttccaaagagtgcccgctgcgcagcgagagatgccaacttcccaaa 120
    |||
Db 194 gctgctctgtctcttccaaagagtgcccgctgcgcagcgagagatgccaacttcccaaa 253

QY 121 gctatgacaacgtgacggtccgcgcaggggagagcgccaccctcaggtgcactatgac 180
    |||
Db 254 gctatgacaacgtgacggtccgcgcaggggagagcgccaccctcaggtgcactatgac 313
```

QY	181	aaccggygtacaccgggtgtgccttgcgttaaacccgacgacacatccttatgtctggyaatgac	240
Db	314	aaccggygtacaccgggtgtgccttgcgttaaacccgacgacacatccttatgtctggyaatgac	373
QY	241	aagtggtgtccttgatctcctcggtgtgtcctctcttgagcaaacacccaacgagtlacagatc	300
Db	374	aagtggtgtccttgatctcctcggtgtgtcctctcttgagcaaacacccaacgagtlacagatc	433
QY	301	gagatccagaacgttgatgtgtatgacgagggccctaacctgtcgttgacagacgac	360
Db	434	gagatccagaacgttgatgtgtatgacgagggccctaacctgtcgttgacagacgac	493
QY	361	aaccaccccaaaagacctctaggtccacctcatltgtgcaagtatctccaaaattgttagag	420
Db	494	aaccaccccaaaagacctctaggtccacctcatltgtgcaagtatctccaaaattgttagag	553
QY	421	attctctcagatatctccatlaatgaagggaaacaatatatagcctcaacctgcatagcaact	480
Db	554	attctctcagatatctccatlaatgaagggaaacaatatatagcctcaacctgcatagcaact	613
QY	481	ggtagaccagagcgcctacggttactcttgagacacatctctccaaaagcggltggttgtg	540
Db	614	ggtagaccagagcgcctacggttactcttgagacacatctctccaaaagcggltggttgtg	673
QY	541	agtgaaagacgaatacttggaaattcaggggcatacccccggagcagtcaggggactacgag	600
Db	674	agtgaaagacgaatacttggaaattcaggggcatacccccggagcagtcaggggactacgag	733
QY	601	tgcagtgctctccaatgacgtgtgcgcgcgcgcggtgtgtacggagagtaaggtcacccgtgaac	660
Db	734	tgcagtgctctccaatgacgtgtgcgcgcgcgcggtgtgtacggagagtaaggtcacccgtgaac	793
QY	661	tatccaccatacatcttcagaaagccaaggggtacaggtgtccccgttggacaaaaaggggaca	720
Db	794	tatccaccatacatcttcagaaagccaaggggtacaggtgtccccgttggacaaaaaggggaca	853
QY	721	ctgcagtgltgaagcctcagcagtcctccctcagcagaattccagtygtacaaggatgaca	780
Db	854	ctgcagtgltgaagcctcagcagtcctccctcagcagaattccagtygtacaaggatgaca	913
QY	781	agactgatctgaaggaagaaaggggtgaaagtggaaaaacagaccttccctcacaac	840
Db	914	agactgatctgaaggaagaaaggggtgaaagtggaaaaacagaccttccctcacaac	973
QY	841	atctcttcaatgtctctgaacatgactatgggaaactacacattgctgtgcctccaacaag	900
Db	974	atctcttcaatgtctctgaacatgactatgggaaactacacattgctgtgcctccaacaag	1033
QY	901	ctgggcacacccaatgtgccagcatatgtctattgtgtccagggcgctcagcgaggtgagc	960
Db	1034	ctgggcacacccaatgtgccagcatatgtctattgtgtccagggcgctcagcgaggtgagc	1093
QY	961	aacggcaccgtcgaggaagggcaggtcgtctgtgctgtcctctctgtctgtgacacctg	1020
Db	1094	aacggcaccgtcgaggaagggcaggtcgtctgtgctgtcctctctgtctgtgacacctg	1153
QY	1021	ctctcacaattt 1032	
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RESULT 4
US-09-918-585A-522
; Sequence 522, Application US/09918585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

```

1  APPLICANT: Gao, Wei-Qiang
2  APPLICANT: Gerber, Hanspeter
3  APPLICANT: Gerritsen, Mary E.
4  APPLICANT: Goddard, Audrey
5  APPLICANT: Godowski, Paul J.
6  APPLICANT: Grimaldi, J. Christopher
7  APPLICANT: Gurney, Austin L.
8  APPLICANT: Hillan, Kenneth J.
9  APPLICANT: Kljavin, Ivar J.
10 APPLICANT: Kuo, Sophia S.
11 APPLICANT: Napier, Mary A.
12 APPLICANT: Pan, James;
13 APPLICANT: Paoni, Nicholas F.
14 APPLICANT: Roy, Margaret Ann
15 APPLICANT: Shelton, David L.
16 APPLICANT: Stewart, Timothy A.
17 APPLICANT: Tumas, Daniel
18 APPLICANT: Williams, P. Mickey
19 APPLICANT: Wood, William I.
20 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
21 TITLE OF INVENTION: Acids Encoding the Same
22 FILE REFERENCE: P2630P1C1
23 CURRENT APPLICATION NUMBER: US/09/918,585A
24 CURRENT FILING DATE: 2001-07-30
25 PRIOR APPLICATION NUMBER: 60/062250
26 PRIOR FILING DATE: 1997-10-17
27 PRIOR APPLICATION NUMBER: 60/064249
28 PRIOR FILING DATE: 1997-11-03
29 PRIOR APPLICATION NUMBER: 60/065311
30 PRIOR FILING DATE: 1997-11-13
31 PRIOR APPLICATION NUMBER: 60/066364
32 PRIOR FILING DATE: 1997-11-21
33 PRIOR APPLICATION NUMBER: 60/077450
34 PRIOR FILING DATE: 1998-03-10
35 PRIOR APPLICATION NUMBER: 60/077632
36 PRIOR FILING DATE: 1998-03-11
37 PRIOR APPLICATION NUMBER: 60/077641
38 PRIOR FILING DATE: 1998-03-11
39 PRIOR APPLICATION NUMBER: 60/077649
40 PRIOR FILING DATE: 1998-03-11
41 PRIOR APPLICATION NUMBER: 60/077791
42 PRIOR FILING DATE: 1998-03-12
43 PRIOR APPLICATION NUMBER: 60/078004
44 PRIOR FILING DATE: 1998-03-13
45 PRIOR APPLICATION NUMBER: 60/078886
46 PRIOR FILING DATE: 1998-03-20
47 PRIOR APPLICATION NUMBER: 60/078936
48 PRIOR FILING DATE: 1998-03-20
49 PRIOR APPLICATION NUMBER: 60/078910
50 PRIOR FILING DATE: 1998-03-20
51 PRIOR APPLICATION NUMBER: 60/078939
52 PRIOR FILING DATE: 1998-03-20
53 PRIOR APPLICATION NUMBER: 60/079294
54 PRIOR FILING DATE: 1998-03-25
55 PRIOR APPLICATION NUMBER: 60/079656
56 PRIOR FILING DATE: 1998-03-26
57 PRIOR APPLICATION NUMBER: 60/079664
58 PRIOR FILING DATE: 1998-03-27
59 PRIOR APPLICATION NUMBER: 60/079689
60 PRIOR FILING DATE: 1998-03-27
61 PRIOR APPLICATION NUMBER: 60/079663
62 PRIOR FILING DATE: 1998-03-27
63 PRIOR APPLICATION NUMBER: 60/079728
64 PRIOR FILING DATE: 1998-03-27
65 PRIOR APPLICATION NUMBER: 60/079786
66 PRIOR FILING DATE: 1998-03-27
67 PRIOR APPLICATION NUMBER: 60/079920
68 PRIOR FILING DATE: 1998-03-30
69 PRIOR APPLICATION NUMBER: 60/079923
70 PRIOR FILING DATE: 1998-03-30
71 PRIOR APPLICATION NUMBER: 60/080105
72 PRIOR FILING DATE: 1998-03-31
73 PRIOR APPLICATION NUMBER: 60/080107

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;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR FILING DATE: 1998-04-30

;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086023
;; PRIOR FILING DATE: 1998-05-18

Query Match 100.0%; Score 1032; DB 34; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaaatgacaattctatctcttggcaatcttcaaggcctg 60
Db 134 atgaaaaccatccagccaaaatgacaattctatctcttggcaatcttcaaggcctg 193
QY 61 gctgctctgtctcttccaagagtgcccgtygcgcagcgagatgccaacttcccaaa 120
Db 194 gctgctctgtctcttccaagagtgcccgtygcgcagcgagatgccaacttcccaaa 253
QY 121 gctatgacaacgtgacggtccgcaggggagagcgccaccctcaagtgactatgac 180
Db 254 gctatgacaacgtgacggtccgcaggggagagcgccaccctcaagtgactatgac 313
QY 181 aaccggtccacccggtgctgctgctaaacgcagcaccaatctctatgtctggaatgac 240
Db 314 aaccggtccacccggtgctgctgctaaacgcagcaccaatctctatgtctggaatgac 373
QY 241 aagtgtgctgctgctcctcgctgctgctctctgagcaaacccaaacgcagtaacgac 300
Db 374 aagtgtgctgctgctcctcgctgctgctctctgagcaaacccaaacgcagtaacgac 433
QY 301 gagatccagaacgtgagatgtatgacagggcccttaacactgtctcgtgacagagac 360
Db 434 gagatccagaacgtgagatgtatgacagggcccttaacactgtctcgtgacagagac 493

QY 361 aaccacccaagaacctctaggtgtccacctctattgtgcaagtatctcccaaaattgttagag 420
|||||
Db 494 aaccacccaagaacctctaggtgtccacctctattgtgcaagtatctcccaaaattgttagag 553
QY 421 attcttcagatatctccatgaatgaagggaacaatatagcctcacctgtacagaact 480
|||||
Db 554 attcttcagatatctccatgaatgaagggaacaatatagcctcacctgtacagaact 613
QY 481 ggtagaccagagcctacgttacttggagacacatctctcccaagcgttggcttgtg 540
|||||
Db 614 ggtagaccagagcctacgttacttggagacacatctctcccaagcgttggcttgtg 673
QY 541 agtgaagacgaataacttggaaattcagggcatacccccggagcagtcaggggactagag 600
|||||
Db 674 agtgaagacgaataacttggaaattcagggcatacccccggagcagtcaggggactagag 733
QY 601 tgcagtgccctcccaatgacgtgtgcccgcgcctgtgtacggagagtaaaagttccagtgtaac 660
|||||
Db 734 tgcagtgccctcccaatgacgtgtgcccgcgcctgtgtacggagagtaaaagttccagtgtaac 793
QY 661 tatccaccatacatttcagaagccaagggtacaggtgtcccccgttgggacaaaaggggaca 720
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Db 794 tatccaccatacatttcagaagccaagggtacaggtgtcccccgttgggacaaaaggggaca 853
QY 721 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacagaatgacaaa 780
|||||
Db 854 ctgcagtgtaagcctcagcagtcctccctcagcagaattccagtggtacagaatgacaaa 913
QY 781 agactgatitgaaggaaagaaagggtgaaggtggaanaacagaccttccctcaaaactc 840
|||||
Db 914 agactgatitgaaggaaagaaagggtgaaggtggaanaacagaccttccctcaaaactc 973
QY 841 atcttcttcaatgtctctgaacatgactatgggaaactacacttgcgttgcctccacaag 900
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Db 974 atcttcttcaatgtctctgaacatgactatgggaaactacacttgcgttgcctccacaag 1033
QY 901 ctgggccacacccaatgcccagcatgtctatttgggtccaggcgcctcagcaggtgagc 960
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Db 1034 ctgggccacacccaatgcccagcatgtctatttgggtccaggcgcctcagcaggtgagc 1093
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Db 1094 aacggcacgtcgaggaaggcagcgtgctgtcgtcgtcgtccttctgtgtttgacctg 1153
QY 1021 ctctcaaat 1032
|||||
Db 1154 ctctcaaat 1165

RESULT 5
US-09-978-188A-522
; Sequence 522, Application US/09978188A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C8
; CURRENT APPLICATION NUMBER: US/09/978,188A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-03-10
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 9.5e-288;
 Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaaatgacaaatctctctcttgagcaatcttcagggtgctg 60
 Db 134 atgaaaaccatccagccaaaatgacaaatctctctcttgagcaatcttcagggtgctg 193
 QY 61 gctgctctgtctcttccaagagtgcccgctgcagcgagatgacaccccca 120
 Db 194 gctgctctgtctcttccaagagtgcccgctgcagcgagatgacaccccca 253
 QY 121 gctatgacaacgtgacggtcccgaggggagagcgccaccctcagtgcactatgac 180
 Db 254 gctatgacaacgtgacggtcccgaggggagagcgccaccctcagtgcactatgac 313
 QY 181 aaccgggtcaccgggtggtgctggttaaacccgagcaccatctctatgctgggaatgac 240
 Db 314 aaccgggtcaccgggtggtgctggttaaacccgagcaccatctctatgctgggaatgac 373
 QY 241 aagtgtgctgtgctctcctgcgtgtgtccttctgagcaacaccccaaacgcagtaacgac 300
 Db 374 aagtgtgctgtgctctcctgcgtgtgtccttctgagcaacaccccaaacgcagtaacgac 433
 QY 301 gagatccagaacgtgagtgatgtgtgacgagggcccttaacacgtgctggtgacagagac 360
 Db 434 gagatccagaacgtgagtgatgtgtgacgagggcccttaacacgtgctggtgacagagac 493
 QY 361 aaccacccaaagacctctaggtgacacctcatgtgcaagtatctcccaaatgttagag 420
 Db 494 aaccacccaaagacctctaggtgacacctcatgtgcaagtatctcccaaatgttagag 553
 QY 421 attctcagatctctccatctaagaggaacaatatagcctcaccgtgacatagcaact 480
 Db 554 attctcagatctctccatctaagaggaacaatatagcctcaccgtgacatagcaact 613
 QY 481 ggtagaccagagcctacggttactgtgagagacacatctctcccaaacgcgtgtgcttgtg 540
 Db 614 ggtagaccagagcctacggttactgtgagagacacatctctcccaaacgcgtgtgcttgtg 673

QY 541 agtgaagcagaatacttggaattcaggcattaccgggagcagtcaggggactacag 600
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Db 674 agtgaagcagaatacttggaattcaggcattaccgggagcagtcaggggactacag 733
QY 601 tgcagtgctcccaatgacgtgcccgcgcccctgtgtacggagagtaaaagtcaccgtgaac 660
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Db 734 tgcagtgctcccaatgacgtgcccgcgcccctgtgtacggagagtaaaagtcaccgtgaac 793
QY 661 tatccaccatacatttcagaagccaaagggtacaggtgtcccccgtggtgacaaaaggggagaca 720
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Db 794 tatccaccatacatttcagaagccaaagggtacaggtgtcccccgtggtgacaaaaggggagaca 853
QY 721 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtgtagacaagatgacaaa 780
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Db 854 ctgcagtgtagaagcctcagcagtcctccctcagcagaattccagtgtagacaagatgacaaa 913
QY 781 agactgattgaaggaagaagggtgaagtggaagacagaccttcctctcaaaactc 840
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Db 914 agactgattgaaggaagaagggtgaagtggaagacagaccttcctctcaaaactc 973
QY 841 atcttctcaatgtctctgaacatgactatggtggaactacacttggtggtcctccaacag 900
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Db 974 atcttctcaatgtctctgaacatgactatggtggaactacacttggtggtcctccaacag 1033
QY 901 ctggggccacacccaatgcccagcatcatgtatttgtccaggcgccgtcagcyaggtgagc 960
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Db 1034 ctggggccacacccaatgcccagcatcatgtatttgtccaggcgccgtcagcyaggtgagc 1093
QY 961 aacggcacgctcagggagggcagcgtgctgtgctgctcctctctgtccttgcacctg 1020
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Db 1094 aacggcacgctcagggagggcagcgtgctgtgctgctcctctctgtccttgcacctg 1153
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Db 1154 ctctccaattt 1165

RESULT 6
US-09-978-189-522
; Sequence 522, Application US/09978189
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaacacatcagccaaatgacacattctctcttgggcaatcttcacgggctg 60
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QY 61 gctcctctgtctctctccaaagagtgcccgctgcgcagcgagatgccaccttcccaaa 120
Db 194 gctcctctgtctctctccaaagagtgcccgctgcgcagcgagatgccaccttcccaaa 253
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QY 181 aaccgggtcacccgggtggtcgtgctaaccgcagcaccaatctctatgttggatggac 240
Db 314 aaccgggtcacccgggtggtcgtgctaaccgcagcaccaatctctatgttggatggac 373
QY 241 aagtggtgcctgtgatatctcgcgtgtctctctgagcaacccaacgaggtacagcacc 300
Db 374 aagtggtgcctgtgatatctcgcgtgtctctctgagcaacccaacgaggtacagcacc 433
QY 301 gagatccagaacgtgatgtgtatgacgagggcccttacacctgtcgtgacagacagac 360
Db 434 gagatccagaacgtgatgtgtatgacgagggcccttacacctgtcgtgacagacagac 493
QY 361 aaccacccaagacctctaggtgccacctctatgtgcagttatctcccaaatgttagag 420
Db 494 aaccacccaagacctctaggtgccacctctatgtgcagttatctcccaaatgttagag 553
QY 421 attcttcagatatctccatlaatgaagggaacaatatlagcctcacctgcatagcaact 480
Db 554 attcttcagatatctccatlaatgaagggaacaatatlagcctcacctgcatagcaact 613
QY 481 gtagacacagagcctaaggttacttggagacacatctctccaaagcggtgtgtgtg 540
Db 614 gtagacacagagcctaaggttacttggagacacatctctccaaagcggtgtgtgtg 673
QY 541 agtgaagcgaatacttgaattcagggcaccacccgggagcagtcaggggactagag 600
Db 674 agtgaagcgaatacttgaattcagggcaccacccgggagcagtcaggggactagag 733
QY 601 tgcagtgctccaatgacgtggtgcgcgcgcctgtgttacggaagtaaaaggtcacccgtgaac 660
Db 734 tgcagtgctccaatgacgtggtgcgcgcgcctgtgttacggaagtaaaaggtcacccgtgaac 793
QY 661 tatccaccatacatctcagaagcgaaggtgtacaggtgtcccggtggacaagaaggagaca 720
Db 794 tatccaccatacatctcagaagcgaaggtgtacaggtgtcccggtggacaagaaggagaca 853

QY 721 ctgcagtgtgaagctcagcagtcctccctcagcagaattccagtggtacaaagtacaaa 780
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 QY 781 agactgattgaagaaagaagggtgaagaagtgaaaaacagaccttctctcaaaactc 840
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 Db 914 agactgattgaagaaagaagggtgaagaagtgaaaaacagaccttctctcaaaactc 973
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 Db 974 atctctcaatgtctctgaacatgactatggaactacacttcgtgcctccaacaag 1033
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 Db 1034 ctgggcacacccaatgccaagcatgctatttggtccaggcgccgtcagcgagtgagc 1093
 QY 961 aacggcagctcgaggaggcgagcgtgctgtgctgctctctctgtgcttcgacctg 1020
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 Db 1094 aacggcagctcgaggaggcgagcgtgctgtgctgctctctctgtgcttcgacctg 1153
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 Db 1154 ctctcaattt 1165

RESULT 7

US-09-978-191A-522

; Sequence 522, Application us/09978191A

; GENERAL INFORMATION:

; APPLICANT: Asikenzai, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C4
 ; CURRENT APPLICATION NUMBER: US/09/978,191A

; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 9.5e-288;
 Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaccatccagccaaaatgcacaaattctcttggcaatcttcagggctg 60
 Db 134 atgaaaccatccagccaaaatgcacaaattctcttggcaatcttcagggctg 193
 QY 61 gctgctctgtctcttccaaaggagtgcccggtgcagcgagatgccaacttcccaaa 120
 Db 194 gctgctctgtctcttccaaaggagtgcccggtgcagcgagatgccaacttcccaaa 253
 QY 121 gctatgacaacgtgacggtccgcaaggaggagagcgccaccctcaggtgcaattgac 180
 Db 254 gctatgacaacgtgacggtccgcaaggaggagagcgccaccctcaggtgcaattgac 313
 QY 181 aaccgggtcaccgggtgctgctgctaaaccgagcaccatcctctatgttggaatgac 240
 Db 314 aaccgggtcaccgggtgctgctgctaaaccgagcaccatcctctatgttggaatgac 373
 QY 241 aagtgtgctgtgatactctcggtgtgtctcttctgagcaaacccaaacgagtagacatc 300
 Db 374 aagtgtgctgtgatactctcggtgtgtctcttctgagcaaacccaaacgagtagacatc 433
 QY 301 gatatccagaacgtgatatgtatgacgaggcccttacacctgtctgtgcagacgac 360
 Db 434 gatatccagaacgtgatatgtatgacgaggcccttacacctgtctgtgcagacgac 493
 QY 361 aaccacccaaaacacctctaggtgccacctattgtcagaatatctcccaaatgttag 420
 Db 494 aaccacccaaaacacctctaggtgccacctattgtcagaatatctcccaaatgttag 553
 QY 421 attcttcagatatctccaaatgaaggaaacaatatagcctcaccctgcatagcaact 480
 Db 554 attcttcagatatctccaaatgaaggaaacaatatagcctcaccctgcatagcaact 613
 QY 481 ggtagaccagagctacggttacttggaagacacatctctccaaagcgttgcttg 540
 Db 614 ggtagaccagagctacggttacttggaagacacatctctccaaagcgttgcttg 673
 QY 541 agtgaagcagaacttggaattcagggcaccacccggagcagtcaggggactagag 600
 Db 674 agtgaagcagaacttggaattcagggcaccacccggagcagtcaggggactagag 733
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 Db 734 tgcagtgccctccaatgacgtgcccgcgcgtgtgtaaggagtaaggtcacccgtgac 793
 QY 661 tatccacatacatcttcagaagccaagggtacaggtgtcccgtyggaaaaaaggagaca 720
 Db 794 tatccacatacatcttcagaagccaagggtacaggtgtcccgtyggaaaaaaggagaca 853
 QY 721 ctgcagtytgaagcctcagcagtcctccctcagcagaattccagtygtacaaagtacaaa 780
 Db 854 ctgcagtytgaagcctcagcagtcctccctcagcagaattccagtygtacaaagtacaaa 913
 QY 781 agactgattgaagaaagaaaggggtgaaggtgnaaaacagaccttctctcaaaatc 840
 Db 914 agactgattgaagaaagaaaggggtgaaggtgnaaaacagaccttctctcaaaatc 973
 QY 841 atcttctcaatgtctctgacaatgactatggaactacacttgctgtgctccaacag 900
 Db 974 atcttctcaatgtctctgacaatgactatggaactacacttgctgtgctccaacag 1033

QY 901 ctggccacccatgcccagcatcatgtattgtgccagggcgccgtcagcgaggtgagc 960
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Db 1034 ctggccacccatgcccagcatcatgtattgtgccagggcgccgtcagcgaggtgagc 1093
QY 961 aacggcagctcgagagggcagcgtcgtctgtcgtcctctctgtctgtctgacctg 1020
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Db 1094 aacggcagctcgagagggcagcgtcgtctgtcgtcctctctgtctgtctgacctg 1153
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Db 1154 ctctcaattt 1165

RESULT 8
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; Sequence 522, Application US/09978192
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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28	PRIOR APPLICATION NUMBER: 60/084366
29	PRIOR FILING DATE: 1998-05-05
30	PRIOR APPLICATION NUMBER: 60/084414
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39	PRIOR FILING DATE: 1998-05-07
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66	PRIOR APPLICATION NUMBER: 60/085704
67	PRIOR FILING DATE: 1998-05-15
68	PRIOR APPLICATION NUMBER: 60/085697
69	PRIOR FILING DATE: 1998-05-15

Query Match	100.0%;	Score 1032;	DB 36;	Length 1679;
Best local Similarity	100.0%;	Pred. No. 9.5e-288;		
Matches 1032;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	134	atgtaaaaccatccagccaaaatgcaaatctatctcttggcaatctcaagggtg	193
QY	61	gctgctctgtgtctcttccaagagtgcgcgtgcgagcgagatgccaacttcccaaa	120
Db	194	gctgctctgtgtctcttccaagagtgcgcgtgcgagcgagatgccaacttcccaaa	253
QY	121	gctatggaacaacgttgaacggtccggcagggggaagcgccacctcaggtgcaattgac	180
Db	254	gctatggaacaacgttgaacggtccggcagggggaagcgccacctcaggtgcaattgac	313
QY	181	aaccggtgtaaccgggttggccttggctaaaacgcagcaaccactctatgtctggaatgac	240
Db	314	aaccggtgtaaccgggttggccttggctaaaacgcagcaaccactctatgtctggaatgac	373
QY	241	aagtgtgtcctgtagctcctcgcgtgtctctcttggacaacaccocaaacgcagtagcatc	300
Db	374	aagtgtgtcctgtagctcctcgcgtgtctctcttggacaacaccocaaacgcagtagcatc	433
QY	301	gagatccagaacacgttgaatgtgtatgacgagggcccttacacctgtcgtgtgcagacagac	360
Db	434	gagatccagaacacgttgaatgtgtatgacgagggcccttacacctgtcgtgtgcagacagac	493
QY	361	aaccacccaaaagacctctaggggtccacctcatgttgcaagtatctccaaaattgtagag	420
Db	494	aaccacccaaaagacctctaggggtccacctcatgttgcaagtatctccaaaattgtagag	553
QY	421	attcttcagatatctccattaatgaagggaacaatatatagcctcacctgcatagcaact	480
Db	554	attcttcagatatctccattaatgaagggaacaatatatagcctcacctgcatagcaact	613
QY	481	ggtagaccagagcgtcctacgttactttggagacacatctctccaaaagcgttggcttgtg	540
Db	614	ggtagaccagagcgtcctacgttactttggagacacatctctccaaaagcgttggcttgtg	673
QY	541	agtgaagacgaatactttgaaattccagggcatcccccggagcagtcaggggactacgag	600
Db	674	agtgaagacgaatactttgaaattccagggcatcccccggagcagtcaggggactacgag	733
QY	601	tgcagttgcttccaatgacgttgcgcgcgtgtgtacggaagttaaagttcacccgtgaac	660
Db	734	tgcagttgcttccaatgacgttgcgcgcgtgtgtacggaagttaaagttcacccgtgaac	793
QY	661	tatccaccatatacttcaagaagccaaaggttacaggtgtccccgttggacaaaaggggaca	720
Db	794	tatccaccatatacttcaagaagccaaaggttacaggtgtccccgttggacaaaaggggaca	853
QY	721	ctgcaggtgtgaagccttcagcagttccccctcagcagaattccagttgtacaaggtatgacaa	780
Db	854	ctgcaggtgtgaagccttcagcagttccccctcagcagaattccagttgtacaaggtatgacaa	913
QY	781	agactgattgaaggaagaaggggtgaaagtgtgaaacagacacttctcttcaaaactc	840
Db	914	agactgattgaaggaagaaggggtgaaagtgtgaaacagacacttctcttcaaaactc	973
QY	841	atcttctcaaatgtctctgaacaatgactatggaactatacactgtgtgacctcaacaag	900
Db	974	atcttctcaaatgtctctgaacaatgactatggaactatacactgtgtgacctcaacaag	1033
QY	901	ctgggccaacccaatgccaagcatcatgtctatttggttccaggcgccgttcagcgaggtgagc	960
Db	1034	ctgggccaacccaatgccaagcatcatgtctatttggttccaggcgccgttcagcgaggtgagc	1093
QY	961	aacggcaacgtcgaaggaggcgagcgtgtctgtgctgtgcctcttctgttcttgcaactg	1020
Db	1094	aacggcaacgtcgaaggaggcgagcgtgtctgtgctgtgcctcttctgttcttgcaactg	1153
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Db	1154	cttctcaaatctt 1165	

RESULT 9
US-09-978-192A-522
; Sequence 522, Application US/09978192A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/077791
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;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaaccatccagccaaatgtcacattctctcttgaggcaatcttcaagggtc 60
Db 134 atgaaaaccatccagccaaatgtcacattctctcttgaggcaatcttcaagggtc 193
QY 61 gctgctctgtctctctccaaggagtgccgtgagcgagcgagatgccaacttcccaaa 120
Db 194 gctgctctgtctctctccaaggagtgccgtgagcgagcgagatgccaacttcccaaa 253
QY 121 gctatgacaacgtgacggtccgaggggagagcgccaacctcaagtgcactattgac 180
Db 254 gctatgacaacgtgacggtccgaggggagagcgccaacctcaagtgcactattgac 313

QY 181 aaccggtgtaaccgggtgtgcttggtctaaaccgagcaaccatctctatgtgtgggaatgac 240
Db 314 aaccggtgtaaccgggtgtgcttggtctaaaccgagcaaccatctctatgtgtgggaatgac 373
QY 241 aagtgtgctgtagctctcgtgtgtctctcttgagcaacacccaaacgagtagagc 300
Db 374 aagtgtgctgtagctctcgtgtgtctctcttgagcaacacccaaacgagtagagc 433
QY 301 gagatccagaacgtgtgatgtatgacgagggccctaacactgtctgtgtgagacagac 360
Db 434 gagatccagaacgtgtgatgtatgacgagggccctaacactgtctgtgtgagacagac 493
QY 361 aaccacccaaagacctctaggtgtccacctattgtgcaagtatctccaaattgtagag 420
Db 494 aaccacccaaagacctctaggtgtccacctattgtgcaagtatctccaaattgtagag 553
QY 421 attcttcaagatatctccattaatgaaaggaacaatatattagcctcactgtgatagcaact 480
Db 554 attcttcaagatatctccattaatgaaaggaacaatatattagcctcactgtgatagcaact 613
QY 481 ggtagaccagagcgtacgttactgtgagacacatctctccaaagcgtgtgtgtg 540
Db 614 ggtagaccagagcgtacgttactgtgagacacatctctccaaagcgtgtgtgtg 673
QY 541 agtgaagacgaatacttggaaattcagggtacacccggagcagtcagggtgactagag 600
Db 674 agtgaagacgaatacttggaaattcagggtacacccggagcagtcagggtgactagag 733
QY 601 tgcagtgtcctccaatgtacgtgtgcccgcgcctgtgtacgagagtaaggtcaacgtgac 660
Db 734 tgcagtgtcctccaatgtacgtgtgcccgcgcctgtgtacgagagtaaggtcaacgtgac 793
QY 661 tatccacatacatctcagaagaaggggtacaggtgttcccggtggtgacaaaggagaca 720
Db 794 tatccacatacatctcagaagaaggggtacaggtgttcccggtggtgacaaaggagaca 853
QY 721 ctgcagtgtgaagcctcagcaggtccctcagcagaattccaggtgttacaaggatgacaa 780
Db 854 ctgcagtgtgaagcctcagcaggtccctcagcagaattccaggtgttacaaggatgacaa 913
QY 781 agactgattgaaggaagaaggggtgaaagtggaaacacagaccttctctcaaaactc 840
Db 914 agactgattgaaggaagaaggggtgaaagtggaaacacagaccttctctcaaaactc 973
QY 841 atcttcttaaatgtctctcgaacatgtacatgtggaactgtgactgtgtgtgtccaaag 900
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QY 901 ctggtgcaacccaatgtccagcatcatgtctattgtgtccaggcgccgtcagcgaggtgagc 960
Db 1034 ctggtgcaacccaatgtccagcatcatgtctattgtgtccaggcgccgtcagcgaggtgagc 1093
QY 961 aacggcacgtcagaggaaggcaggtgcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Db 1094 aacggcacgtcagaggaaggcaggtgcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1153
QY 1021 ctctcaaat 1032
Db 1154 ctctcaaat 1165

RESULT 10
US-09-978-193A-522
; Sequence 522, Application US/09978193A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C6
CURRENT APPLICATION NUMBER: US/09/978,193A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gctgctctgtctcttccaagagtgcccgctgcgcagcgagatgccaacttcccaaa 120
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Db 194 gctgctctgtctcttccaagagtgcccgctgcgcagcgagatgccaacttcccaaa 253

QY 121 gctatggacaacgtgacggtccggcaggggagagcgccaccctcaagtgcaactatggac 180
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Db 254 gctatggacaacgtgacggtccggcaggggagagcgccaccctcaagtgcaactatggac 313

QY 181 aaccgggtcaccgggtgctgctgcttaaacccgacgaccatctctatgtctgggaatgac 240
|||||
Db 314 aaccgggtcaccgggtgctgctgcttaaacccgacgaccatctctatgtctgggaatgac 373

QY 241 aagtgtgcttgatctctcgcgtgtgtcctcttgagcaacacccaaacgacgtacagcatc 300
|||||
Db 374 aagtgtgcttgatctctcgcgtgtgtcctcttgagcaacacccaaacgacgtacagcatc 433

QY 301 gagatccagaacgtgatgtgtatagcagagggcccttacacactgtcgtgtgcagacagac 360
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Db 434 gagatccagaacgtgatgtgtatagcagagggcccttacacactgtcgtgtgcagacagac 493

QY 361 aaccaccaagacctaggtgccacctcaattgtgcaagtatctccaaaattgtagag 420
|||||
Db 494 aaccaccaagacctaggtgccacctcaattgtgcaagtatctccaaaattgtagag 553

QY 421 attcttcaatatcttccattaatgaagggaacaaratatagcctcaactgcatagcaact 480
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Db 554 attcttcaatatcttccattaatgaagggaacaaratatagcctcaactgcatagcaact 613

QY 481 ggtagaaccagacctagcgttacttctgagacacatctctccaaagcgttggcttgtg 540
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Db 614 ggtagaaccagacctagcgttacttctgagacacatctctccaaagcgttggcttgtg 673

QY 541 agtgaagacgaatacttggaaattcaaggcatcacccggagcagtcagggactacgag 600
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Db 674 agtgaagacgaatacttggaaattcaaggcatcacccggagcagtcagggactacgag 733

QY 601 tgcagtgccctccaatgacgttgcgcgcgcgtgtgtaagagtaaggtcaccggtgac 660
|||||
Db 734 tgcagtgccctccaatgacgttgcgcgcgcgtgtgtaagagtaaggtcaccggtgac 793

QY 661 tatccaccatacatcttcagaagccaaaggtacaggtgtcccgctgggacaagaaggagaca 720
|||||
Db 794 tatccaccatacatcttcagaagccaaaggtacaggtgtcccgctgggacaagaaggagaca 853

QY 721 ctgcagtggtgaagcctcagcagctccctcagcagaattccagtggtacaaagtgacaaa 780
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Db 854 ctgcagtggtgaagcctcagcagctccctcagcagaattccagtggtacaaagtgacaaa 913

QY 781 agactgatgaagaaagaagggtgaaagtggaaaacagaccttctctcaaaatc 840
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Db 914 agactgatgaagaaagaagggtgaaagtggaaaacagaccttctctcaaaatc 973

QY 841 atctcttcaatgctctgaaactgacttggaaactacacttgcgtgcctccaagaag 900
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Db 974 atctcttcaatgctctgaaactgacttggaaactacacttgcgtgcctccaagaag 1033

QY 901 ctgggccacacccaatgccaagcatcatgtattgtgccagcgccgtcagcgaggtgagc 960
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Db 1034 ctgggccacacccaatgccaagcatcatgtattgtgccagcgccgtcagcgaggtgagc 1093

QY 961 aacggacgctcgaggaaggcgagcgtgcgtctgctgctgcctctctgtcttgcacctg 1020
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Db 1094 aacggacgctcgaggaaggcgagcgtgcgtctgctgctgcctctctgtcttgcacctg 1153

QY 1021 ctctcaaat 1032
|||
Db 1154 ctctcaaat 1165

RESULT 11
US-09-978-194A-522
; Sequence 522, Application US/09978194A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fliviaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC10
 ; CURRENT APPLICATION NUMBER: US/09/978,194A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15

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Query Match      100.0%; Score 1032; DB 36; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gctgctctgtctctccaaggagtgcccggtcgagcgagatgcccactccccaaa 120
Db 194 gctgctctgtctctccaaggagtgcccggtcgagcgagatgcccactccccaaa 253
QY 121 gctatgacacagtgacggtccgaggggagagcgccacctcagtgacattgac 180
Db 254 gctatgacacagtgacggtccgaggggagagcgccacctcagtgacattgac 313
QY 181 aaccgggtcacccgggtggtcgtgtaaacccgagcaccatctctatgtctgggaatgac 240
Db 314 aaccgggtcacccgggtggtcgtgtaaacccgagcaccatctctatgtctgggaatgac 373
QY 241 aagtggtccttgatctctcgtggtgtctctcttgagcaacacccaaacgcagtaacgac 300
Db 374 aagtggtccttgatctctcgtggtgtctctcttgagcaacacccaaacgcagtaacgac 433
QY 301 gagatccagaacgtgtgatacagagggcccttacacctctcgtgtgcagacagac 360
Db 434 gagatccagaacgtgtgatacagagggcccttacacctctcgtgtgcagacagac 493
QY 361 aaccacccaaagaccttaggtgtccacctcatgtgcaagtatctcccaaatgttagag 420
Db 494 aaccacccaaagaccttaggtgtccacctcatgtgcaagtatctcccaaatgttagag 553
QY 421 attcttcagatatctccaattaatgaagggaacaatatagcctcaactgacatgaact 480
Db 554 attcttcagatatctccaattaatgaagggaacaatatagcctcaactgacatgaact 613
QY 481 ggtagaccagagcctacagttacttgagagacacatctctcccaaacggttgcttgtg 540
Db 614 ggtagaccagagcctacagttacttgagagacacatctctcccaaacggttgcttgtg 673

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QY 541 agtgaagacgaatacttggaaattcagggcatacccgaggcagtcaggggactacgag 600
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QY 601 tgcagtgctcccaatgacgtggtcgccggtgtgtaacgagagtaaaagttaacggtgac 660
Db 734 tgcagtgctcccaatgacgtggtcgccggtgtgtaacgagagtaaaagttaacggtgac 793
QY 661 tatccacatacatattcagaagccaaagggtacaggtgtcccggtggacaaaggagaca 720
Db 794 tatccacatacatattcagaagccaaagggtacaggtgtcccggtggacaaaggagaca 853
QY 721 ctgcagtggtgaagcctcagcaggtccctcagcagaattccagtggtacaagatgacaaa 780
Db 854 ctgcagtggtgaagcctcagcaggtccctcagcagaattccagtggtacaagatgacaaa 913
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Db 914 agactgattgaagaaagaaagggtgaaagtggaaacacagaccttctctcaaacctc 973
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QY 901 ctgggccaaccaatgccaagcatcatgtctattgttccaaggcccgctcagcaggtgagc 960
Db 1034 ctgggccaaccaatgccaagcatcatgtctattgttccaaggcccgctcagcaggtgagc 1093
QY 961 aacggcacgtcgaggagggcaggtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Db 1094 aacggcacgtcgaggagggcaggtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1153
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RESULT 12
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; Sequence 522, Application US/09978295A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gernitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James?
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978, 295A

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1 CURRENT FILING DATE: 2001-10-15
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5 PRIOR FILING DATE: 1997-10-17
6 PRIOR APPLICATION NUMBER: 60/064249
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10 PRIOR APPLICATION NUMBER: 60/066364
11 PRIOR FILING DATE: 1997-11-21
12 PRIOR APPLICATION NUMBER: 60/077450
13 PRIOR FILING DATE: 1998-03-10
14 PRIOR APPLICATION NUMBER: 60/077632
15 PRIOR FILING DATE: 1998-03-11
16 PRIOR APPLICATION NUMBER: 60/077641
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30 PRIOR APPLICATION NUMBER: 60/078939
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43 PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
Best Local Similarity 100.0%; Pred. No. 9.5e-288;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 194 gctgctctgtctcttccaaagagtgcccgtygcagcgagatgcccacttcccaa 253
QY 121 gctatgacaacgtgacggtccgaggggagagcgccacccctcaggtgacattgac 180
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QY 181 aaccggtcacccggtgctgctgctaaccgacgacacatctctatgtctgggaatgac 240
Db 314 aaccggtcacccggtgctgctgctaaccgacgacacatctctatgtctgggaatgac 373
QY 241 aagtgtgcttgatcctcgcgtggtcctcttgagcaacacccaaagcagttacagatc 300
Db 374 aagtgtgcttgatcctcgcgtggtcctcttgagcaacacccaaagcagttacagatc 433
QY 301 gagatccagaacgtgatatgacgagggcccttacacctgtgctgctgacagacgac 360
Db 434 gagatccagaacgtgatatgacgagggcccttacacctgtgctgctgacagacgac 493
QY 361 aaccacccaaagacctctaggttccacctatgtgcaatgatactcccaaatgtagag 420
Db 494 aaccacccaaagacctctaggttccacctatgtgcaatgatactcccaaatgtagag 553
QY 421 attctcagatatctccattaatgaagggacaatatattagcctcacctgcatagcaact 480
Db 554 attctcagatatctccattaatgaagggacaatatattagcctcacctgcatagcaact 613
QY 481 gtagaccagagcctaaggttacttggagacacatctctccaaagcggttgcttgty 540
Db 614 gtagaccagagcctaaggttacttggagacacatctctccaaagcggttgcttgty 673
QY 541 agtgaagcgaatacttgaattcagggcaccccgagagcagtcaggsgaactaagag 600
Db 674 agtgaagcgaatacttgaattcagggcaccccgagagcagtcaggsgaactaagag 733
QY 601 tgcagtgcctccaatgacgtgcccgcgcgtgtgtaagagagtaaggtcacccgtgaac 660
Db 734 tgcagtgcctccaatgacgtgcccgcgcgtgtgtaagagagtaaggtcacccgtgaac 793
QY 661 tatccaccatacatctcagaagccaaaggtacaggtgtcccccgtgggacaaaggagaca 720
Db 794 tatccaccatacatctcagaagccaaaggtacaggtgtcccccgtgggacaaaggagaca 853

QY 721 ctgcagtgtgaagcctcagcagtcctccctcagcagaatcccaagtgtgtaacaagtgacaaa 780
Db 854 ctgcagtgtgaagcctcagcagtcctccctcagcagaatcccaagtgtgtaacaagtgacaaa 913
QY 781 agactgattgaagaaagaaaggggtgaaagtgtgaaacagaccccttctctcaaaactc 840
Db 914 agactgattgaagaaagaaaggggtgaaagtgtgaaacagaccccttctctcaaaactc 973
QY 841 atctctcaatgtctctgaacatgactatggaactggaactgctgctgctccaaag 900
Db 974 atctctcaatgtctctgaacatgactatggaactggaactgctgctgctccaaag 1033
QY 901 ctgggccaacccaatgccaacatgataattgttccagcgccgtcagcgagtgagc 960
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Db 1154 ctctccaattt 1165

RESULT 13
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; Sequence 522, Application US/09978298A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C2
; CURRENT APPLICATION NUMBER: US/09/978, 298A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450

1	PRIOR FILING DATE: 1998-03-10
2	PRIOR APPLICATION NUMBER: 60/077632
3	PRIOR FILING DATE: 1998-03-11
4	PRIOR APPLICATION NUMBER: 60/077641
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6	PRIOR APPLICATION NUMBER: 60/077649
7	PRIOR FILING DATE: 1998-03-11
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9	PRIOR FILING DATE: 1998-03-12
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11	PRIOR FILING DATE: 1998-03-13
12	PRIOR APPLICATION NUMBER: 60/078886
13	PRIOR FILING DATE: 1998-03-20
14	PRIOR APPLICATION NUMBER: 60/078936
15	PRIOR FILING DATE: 1998-03-20
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17	PRIOR FILING DATE: 1998-03-20
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19	PRIOR FILING DATE: 1998-03-20
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21	PRIOR FILING DATE: 1998-03-25
22	PRIOR APPLICATION NUMBER: 60/079656
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25	PRIOR FILING DATE: 1998-03-27
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33	PRIOR FILING DATE: 1998-03-27
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36	PRIOR APPLICATION NUMBER: 60/079923
37	PRIOR FILING DATE: 1998-03-30
38	PRIOR APPLICATION NUMBER: 60/080105
39	PRIOR FILING DATE: 1998-03-31
40	PRIOR APPLICATION NUMBER: 60/080107
41	PRIOR FILING DATE: 1998-03-31
42	PRIOR APPLICATION NUMBER: 60/080165
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61	PRIOR FILING DATE: 1998-04-08
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73	PRIOR FILING DATE: 1998-04-15

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6	PRIOR FILING DATE: 1998-04-21
7	PRIOR APPLICATION NUMBER: 60/082704
8	PRIOR FILING DATE: 1998-04-22
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10	PRIOR FILING DATE: 1998-04-22
11	PRIOR APPLICATION NUMBER: 60/082700
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19	PRIOR APPLICATION NUMBER: 60/083322
20	PRIOR FILING DATE: 1998-04-28
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37	PRIOR APPLICATION NUMBER: 60/083500
38	PRIOR FILING DATE: 1998-04-29
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40	PRIOR FILING DATE: 1998-04-30
41	PRIOR APPLICATION NUMBER: 60/084366
42	PRIOR FILING DATE: 1998-05-05
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68	PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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 ; PRIOR APPLICATION NUMBER: 60/085573
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1032; DB 36; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 9.5e-288;
 Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 gctgctctgtctcttccaaagagtgcccggtgcagcgagatgcacactccccaa 120
 Db 194 gctgctctgtctcttccaaagagtgcccggtgcagcgagatgcacactccccaa 253
 QY 121 gctatgacacgtgacggtccgcaggggagagcgccacccctcaggtgcactattgac 180
 Db 254 gctatgacacacgtgacggtccgcaggggagagcgccacccctcaggtgcactattgac 313
 QY 181 aaccgggtcacccgggtgctgctgctaaccgcagccacatctctatgtctgagatgac 240
 Db 314 aaccgggtcacccgggtgctgctgctaaccgcagccacatctctatgtctgagatgac 373
 QY 241 aagtggtgctggtatcctcgctgtgtccttctgagcaacccaaagcagtagacatc 300
 Db 374 aagtggtgctggtatcctcgctgtgtccttctgagcaacccaaagcagtagacatc 433
 QY 301 gagatccagaacgtggtatgtatgacagagggcccttacacctgctggtgacagacac 360
 Db 434 gagatccagaacgtggtatgtatgacagagggcccttacacctgctggtgacagacac 493
 QY 361 aaccacccaaagaccccttagaggtccacctatgtgcaagtatctccaaatgttagag 420
 Db 494 aaccacccaaagaccccttagaggtccacctatgtgcaagtatctccaaatgttagag 553
 QY 421 attcttcagatatctccaatgaagggaaacatatagcctcaccctgacatagcaact 480
 Db 554 attcttcagatatctccaatgaagggaaacatatagcctcaccctgacatagcaact 613
 QY 481 ggtagaccagagcctacggttacttggagacacatctctccaaagcgtgtgttgg 540
 Db 614 ggtagaccagagcctacggttacttggagacacatctctccaaagcgtgtgttgg 673
 QY 541 agtgaagcgaatacttggaaatcagggcatacccgaggagcagtcaggagactagag 600
 Db 674 agtgaagcgaatacttggaaatcagggcatacccgaggagcagtcaggagactagag 733
 QY 601 tgcagtgccctccaatgacgtggtgcgcgcgcgtgtacgagagtaaggtcacccgtgaac 660
 Db 734 tgcagtgccctccaatgacgtggtgcgcgcgcgtgtacgagagtaaggtcacccgtgaac 793
 QY 661 tatccaccatacatctcagaagccaagggtacaggtgtcccggtggacaaaggagaca 720
 Db 794 tatccaccatacatctcagaagccaagggtacaggtgtcccggtggacaaaggagaca 853
 QY 721 ctgcagtgtagagcctcagcagtcctccctcagcagaattccagtggttacaaggtgacaa 780
 Db 854 ctgcagtgtagagcctcagcagtcctccctcagcagaattccagtggttacaaggtgacaa 913
 QY 781 agactgattgaaagaaagaggtgaaagtggaaacacagaccttctctcaaaactc 840
 Db 914 agactgattgaaagaaagaggtgaaagtggaaacacagaccttctctcaaaactc 973
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 Db 974 atcttctcaatgtctctgacacatgctatgggaactacactgtggtggtcccaacaag 1033

QY 901 ctgggcccacacaaatgccagcatcatgtattgtccaggcgcgtcagcgaggtgagc 960
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 QY 1021 ctctcaaat 1032
 Db 1154 ctctcaaat 1165

RESULT 14

US-09-978-299A-522

; Sequence 522, Application US/09978299A

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Flivarov, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC3
 ; CURRENT APPLICATION NUMBER: US/09/978, 299A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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9	PRIOR FILING DATE:	1998-03-25
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11	PRIOR FILING DATE:	1998-03-26
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65	PRIOR APPLICATION NUMBER: 60/085573
66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085704
68	PRIOR FILING DATE: 1998-05-15
69	PRIOR APPLICATION NUMBER: 60/085697
70	PRIOR FILING DATE: 1998-05-15

Query Match	100.0%;	Score 1032;	DB 36;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 9.5e+288;		

Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 194 gctgctctgttctcttccaaggagtgccgctgagcgagagatgccaacttcccaaa 253

QY 121 gctatggacaacgtgacggtccggcgaggggagagcgccacctcaggtgcaactatggac 180
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Db 254 gctatggacaacgtgacggtccggcgaggggagagcgccacctcaggtgcaactatggac 313

QY 181 aaccgggtcacccgggtgagcgtggttaaacccgagcaccactctatgctggaatgac 240
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QY 241 aagtggtgctggtgactctcgcggtgcttctgagcaaccccaaaacgagtagacatc 300
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QY 301 gagatccagaacgtgagtgtatgacgagggcccttacacctgctcggtgacagagac 360
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Db 434 gagatccagaacgtgagtgtatgacgagggcccttacacctgctcggtgacagagac 493

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Db 494 aaccacccaaagaccttaggtgtccacctatgtgcaagtatctccaaaattgtagag 553

QY 421 attcttcagatatctccattaatgaagggaacataattagcctcacctgcaactagcaact 480
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Db 554 attcttcagatatctccattaatgaagggaacataattagcctcacctgcaactagcaact 613

QY 481 ggtagaccagagcctacggttacttgygagacacatctctccaaaagcggttgcttgtg 540
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Db 614 ggtagaccagagcctacggttacttgygagacacatctctccaaaagcggttgcttgtg 673

QY 541 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtcaggagactagag 600
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Db 674 agtgaagacgaatacttggaaattcagggcatcaccgggagcagtcaggagactagag 733

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Db 974 atcttctcaatgtcttgaacaatgactatgaggaactaacttgcgtgctccaacaag 1033

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Db 1034 ctgggccaacacaatgccaacatcatgtatttgtccagcgccgtcagcgaggtgagc 1093

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Db 1094 aacggcacgtcgagagggcgagcgctgctgctgcttcttctgttcttgcaactg 1153

QY 1021 ctctccaattt 1032
    |||||||
Db 1154 ctctccaattt 1165
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RESULT 15
US-09-978-585-522
; Sequence 522, Application US/09978585
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
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; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-585-522

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Db 1154 ctctcaaat 1165

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 23:01:01 ; Search time 435.78 Seconds
(without alignments)
6670.192 Million cell updates/sec

Title: US-09-700-397-2
Perfect score: 1693
Sequence: 1 gtccttcagcaaaacagtgg.....aaaaaaaaaaaaaaaa 1693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1693	100.0	1693	21	AAZ47893	Human protein enco
2	1661.4	98.1	1679	20	AAZ34324	Human PRO337 nucle
3	1661.4	98.1	1679	21	AAC78590	Human PRO337 nucle
4	1661.4	98.1	1679	22	AAS21431	Human CDNA sequenc
5	1661.4	98.1	1679	22	AAC87037	Nucleotide sequenc
6	1625.8	96.0	2012	21	AAA88791	Human SECX CDNA C1
7	1588.8	93.8	1603	21	AAA88790	Human SECX CDNA C1
8	1455.4	86.0	1678	22	AAI57869	Human polynucleoti
9	1297.4	76.6	1690	22	AAI59655	Human polynucleoti

10	1032	61.0	1032	21	AAZ47892	Human protein enco
11	939	55.5	939	21	AAZ47894	Human protein enco
12	787.8	46.5	832	21	AAA44536	Human secreted exp
13	540.8	31.9	3069	14	AAQ51015	Rat opioid recepto
14	523	30.9	2179	14	AAQ51017	Rat opioid recepto
15	523	30.9	2337	14	AAQ51016	Rat opioid recepto
16	503	29.7	503	20	AAZ34325	Human EST DNA42301
17	503	29.7	503	21	AAC78591	Human EST DNA42301
18	475.2	28.1	537	22	AAC91321	Human polynucleoti
19	430.2	25.4	452	22	AAF93346	Spinal cord tissue
20	396	23.4	484	23	AAS78035	DNA encoding novel
21	343	20.3	1238	17	AAT42080	Rat LAMP coding se
22	340.6	20.1	924	17	AAT42084	Human LAMP residue
23	340.6	20.1	977	17	AAT42079	Human LAMP residue
24	340.6	20.1	1014	17	AAT42081	Human LAMP coding se
25	338.6	20.0	861	17	AAT42086	Human LAMP residue
26	338.6	20.0	912	17	AAT42082	Human mature LAMP
27	337.4	19.9	945	17	AAT42085	Human mature LAMP
28	337	19.9	930	17	AAT42083	Rat mature LAMP co
29	333.8	19.7	861	17	AAT42087	Rat LAMP residues
30	331.8	19.6	1307	17	AAT42116	Rat LAMP clone 6c
31	325.2	19.2	1153	22	AAH34425	Human colon cancer
32	316.2	18.7	733	21	AAC19214	Human secreted pro
33	303.6	17.9	756	17	AAT42094	Human LAMP residue
34	298.2	17.6	756	17	AAT42095	Rat LAMP residues
35	296.8	17.5	443	23	AAS78034	DNA encoding novel
36	272.6	16.1	4834	22	AAC87055	Nucleotide sequenc
37	269.4	15.9	2840	21	AAC78596	Human PRO4993 nucl
38	255	15.1	255	20	AAH87585	Human single nucle
39	250.6	14.8	251	19	AAH10694	Human biallelic po
40	240.8	14.2	2813	22	ABA06475	Human CDNA SEQ ID
41	220.6	13.0	4656	22	AAS28811	Human immunoglobul
42	217.8	12.9	2883	23	AAS78003	DNA encoding novel
43	193.6	11.4	352	21	AAC02777	Human secreted pro
44	170.2	10.1	767	23	AAS78037	DNA encoding novel
45	163.2	9.6	585	22	AAF93597	Umbilical vein end

ALIGNMENTS

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AC	AAZ47893;
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DF	10-MAR-2000 (first entry)
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DE	Human protein encoding CDNA SEQ ID NO:3.
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KW	Human; haematopoietic cell regulation; tissue generation; reparation;
KW	activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW	receptor; ligand; autoimmune; infection-related immunodeficiency;
KW	inflammatory disorder; neurological disease; ss.
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XX	
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	CDS
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XX	Location/Qualifiers
XX	214..1164
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PN	W09958668-A1.
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PD	18-NOV-1999.
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PF	13-MAY-1999; 99WO-JP02485.
XX	
PR	14-MAY-1998; 98JP-0131815.
XX	
PA	(ONOI) ONO PHARM CO LTD.
XX	
PI	Fukushima D, Shibayama S, Tada H;

XX WPI: 2000-062298/05.
DR P-PSDB; AAY57601.

XX New polypeptides of human origin having cell regulatory, tissue
PT generation, coagulant and other activities

XX Claim 5; Page 42-45; 84pp; Japanese.

XX The present sequence encodes a specifically claimed novel human protein.
CC The novel human protein can be used in therapeutic drugs for the
CC prevention and treatment of a broad range of disorders including
CC autoimmune and infection-related immunodeficiency, inflammatory
CC disorders, and neurological diseases. The novel protein is expected of
CC having haematopoietic cell regulatory activity, tissue generation/
CC repairation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC blood coagulation and thrombus activity, and receptor/ligand activity.

XX Sequence 1693 BP; 518 A; 432 C; 416 G; 327 T; 0 other;

Query Match 100.0%; Score 1693; DB 21; Length 1693;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID AAZ34324 standard; cDNA; 1679 BP.
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DT	07-DEC-1999	(first entry)
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DE	Human PRO337	nucleotide sequence.
XX		
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KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
XX	secreted protein; transmembrane protein; ss.	
OS	Homo sapiens.	
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PN	WO946281-A2.	
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PD	16-SEP-1999.	
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PF	08-MAR-1999;	99WO-US05028.
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PR	05-MAY-1998;	98US-0084366.
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PR	22-MAY-1998;	98US-0086430.
PR	22-MAY-1998;	98US-0086486.
PR	28-MAY-1998;	98US-0087098.
PR	28-MAY-1998;	98US-0087106.
PR	28-MAY-1998;	98US-0087208.
PR	30-JUL-1998;	98US-0094651.
PR	11-SEP-1998;	98US-0100038.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.
P-PSDB; AAY41773.

New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -

Claim 2; Fig 221; 530pp; English.

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match	98.1%;	Score 1661.4;	DB 20;	Length 1679;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1673; Conservative	0;	Mismatches	1;	Indels 1; Gaps 1;

QY 1 gtccttcagcaaaacagtgatattaatctccttcgcacaaagcttgagagcaacaacatct 60
|||||
Db 6 gtccttcagcaaaacagtgatattaatctccttcgcacaaagcttgagagcaacaacatct 65

QY 61 atcaggaagaagaaagaaagaaaaaacctgcacaaagaaagaaagaaagaa 120
|||||
Db 66 atcaggaagaagaaagaaagaaaaaacctgcacaaagaaagaaagaaagaa 124

QY 121 aaaaalcatgaaaaaccatccagccaaaatgcaaatctctcttgggcaatcttc 180
|||||
Db 125 aaaaaatcatgaaaaaccatccagccaaaatgcaaatctctcttgggcaatcttc 184
QY 181 acgggctgctgtctgtctcttccaaggagtgcccgctgcagcgagatgccaac 240
|||||
Db 185 acgggctgctgtctgtctcttccaaggagtgcccgctgcagcgagatgccaac 244
QY 241 ttccccaagctatggaacaacgctgacggtcccgcaaggaggagcgccacctcagtg 300
|||||
Db 245 ttccccaagctatggaacaacgctgacggtcccgcaaggaggagcgccacctcagtg 304
QY 301 actatgacaacccgggtcaaccgggtggcctggttaaacccgcaaccatctctatg 360
|||||
Db 305 actatgacaacccgggtcaaccgggtggcctggttaaacccgcaaccatctctatg 364
QY 361 gggaatgacaagtggtgctgatacctcgctgcttctctgaagcaacaaccacaacg 420
|||||
Db 365 gggaatgacaagtggtgctgatacctcgctgcttctctgaagcaacaaccacaacg 424
QY 421 tacagcatcgagatccgaacagtgatgtatgacgagggcccttacacctgctcg 480
|||||
Db 425 tacagcatcgagatccgaacagtgatgtatgacgagggcccttacacctgctcg 484
QY 481 cagacagacaaccaccaagaaccttaagggtccacctcatgtgcaagtatcccaaa 540
|||||
Db 485 cagacagacaaccaccaagaaccttaagggtccacctcatgtgcaagtatcccaaa 544
QY 541 attgtagaattctctcagatatctccattaatgaagggaacaatatagcctcac 600
|||||
Db 545 attgtagaattctctcagatatctccattaatgaagggaacaatatagcctcac 604
QY 601 atagcaactgtagaccagaagcctacggttacttgagagacacatctctccaaa 660
|||||
Db 605 atagcaactgtagaccagaagcctacggttacttgagagacacatctctccaaa 664
QY 661 ggcttgtgagtgaaagcaataacttgaaattcagggcatcacccgggagcagtg 720
|||||
Db 665 ggcttgtgagtgaaagcaataacttgaaattcagggcatcacccgggagcagtg 724
QY 721 gactacgagtgagtgctcctccaatgacgtggccgcccgtgtgacgagagtaaa 780
|||||
Db 725 gactacgagtgagtgctcctccaatgacgtggccgcccgtgtgacgagagtaaa 784
QY 781 accgtgaactaccacatacttccagaagccaagggtacaggtgtcccccgtgg 840
|||||
Db 785 accgtgaactaccacatacttccagaagccaagggtacaggtgtcccccgtgg 844
QY 841 aaggggacactgagtgtaagcctcagcaggtccctcagcagaattccagtgta 900
|||||
Db 845 aaggggacactgagtgtaagcctcagcaggtccctcagcagaattccagtgta 904
QY 901 gatgacaaaagactgattgaaagaaaggggtgaagtggaanaacagaccttc 960
|||||
Db 905 gatgacaaaagactgattgaaagaaaggggtgaagtggaanaacagaccttc 964
QY 961 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttg 1020
|||||
Db 965 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttg 1024
QY 1021 tccaacaagctgggccaacccaatgccaagcatgtattgtgccaggcgccg 1080
|||||
Db 1025 tccaacaagctgggccaacccaatgccaagcatgtattgtgccaggcgccg 1084
QY 1081 gaggtgagcaacgcaagtcgaggaaggcgagcgtcgctggctgtgctcttctg 1140
|||||
Db 1085 gaggtgagcaacgcaagtcgaggaaggcgagcgtcgctggctgtgctcttctg 1144
QY 1141 ttgacctgtcttcaaattttgatgtgagtgcaacttcccaaccggggaagcgtg 1200
|||||
Db 1145 ttgacctgtcttcaaattttgatgtgagtgcaacttcccaaccggggaagcgtg 1204

QY 1201 ccaccaccaccaccaccacacagcaatgagcaacaccgacagcaaccatcagatata 1260
|||||
Db 1205 ccaccaccaccaccaccacacagcaatgagcaacaccgacagcaaccatcagatata 1264
QY 1261 caaatgaattagaagaacacagcctcatgagacagaatttgaggagggaacaa 1320
|||||
Db 1265 caaatgaattagaagaacacagcctcatgagacagaatttgaggagggaacaa 1324
QY 1321 aatacttgggggggaaagttttaaaagaatltgaaatgtcgcttcagatatla 1380
|||||
Db 1325 aatacttgggggggaaagagtttaaaagaatltgaaatgtcgcttcagatatla 1384
QY 1381 ggtacaatggagtttcttcttcccaaacggggaagaacacagcacaccggcttg 1440
|||||
Db 1385 ggtacaatggagtttcttcttcccaaacggggaagaacacagcacaccggcttg 1444
QY 1441 ctgcaagctgcatcggtgcaacctcttgggtgcaagtgaggcaaggtcagcct 1500
|||||
Db 1445 ctgcaagctgcatcggtgcaacctcttgggtgcaagtgaggcaaggtcagcct 1504
QY 1501 cccacagagtgcccccagctggaacatctctgagctggccatcccaatcaatcag 1560
|||||
Db 1505 cccacagagtgcccccagctggaacatctctgagctggccatcccaatcaatcag 1564
QY 1561 atagagcagacaagaatgagaccttcggcccaagcgtggcgtcgggacattg 1620
|||||
Db 1565 atagagcagacaagaatgagaccttcggcccaagcgtggcgtcgggacattg 1624
QY 1621 actgtgccaccacagcggtgtgtgtgaaacgtgaaataaaagagcaaaaaa 1675
|||||
Db 1625 actgtgccaccacagcggtgtgtgtgaaacgtgaaataaaagagcaaaaaa 1679

RESULT 3
AAC78590
ID AAC78590 standard; cDNA; 1679 BP.
XX
AC AAC78590;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO337 nucleotide sequence SEQ ID NO:522.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX

PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR MPI; 2000-611443/58.
DR p-PSDB; AAB44329.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 2; Fig 221; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytosolic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 98.1%; Score 1661.4; DB 21; Length 1679;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtccttcagcaaaacagtgatttaattctcttcacaaagcttgagagcaacaatct 60
Db 6 gtccttcagcaaaacagtgatttaattctcttcacaaagcttgagagcaacaatct 65
QY 61 atcaggaagaagaagaagaaaaaaacccgaacctgacaaaaaagaagaagaaga 120
Db 66 atcaggaagaagaagaag-aaaaaacgcgaacctgacaaaaaagaagaagaaga 124
QY 121 aaaaaaatcatgaaacatccagccaaaatgacaaattctatctcttgggcaattctc 180
Db 125 aaaaaaatcatgaaacatccagccaaaatgacaaattctatctcttgggcaattctc 184
QY 181 acggggtgctgtctgtctcttccaaagagtgcccgctgcgcagcgagatgcacc 240
Db 185 acggggtgctgtctgtctcttccaaagagtgcccgctgcgcagcgagatgcacc 244
QY 241 ttccccaagctatggaacacgtgacggtccggcagggggagagcgccaccctcaggtgc 300
Db 245 ttccccaagctatggaacacgtgacggtccggcagggggagagcgccaccctcaggtgc 304
QY 301 actatgacaacccgggtgcacccgggtgctgctgtaaacccgcagcaccatcctatgct 360
Db 305 actatgacaacccgggtgcacccgggtgctgctgtaaacccgcagcaccatcctatgct 364
QY 361 gggaatgacaagtgtgctcgatcctcgctgtgctcttctgagcaaacccaacgcag 420
Db 365 gggaatgacaagtgtgctcgatcctcgctgtgctcttctgagcaaacccaacgcag 424
QY 421 tacagcatcgagatccagaacgttgatgtatgacgagggcccttacacctgctggtg 480
Db 425 tacagcatcgagatccagaacgttgatgtatgacgagggcccttacacctgctggtg 484
QY 481 cagacagacaaccacccaagaacctctaaaggtccacctcattgtgcaagtatatcccaaa 540
Db 485 cagacagacaaccacccaagaacctctaaaggtccacctcattgtgcaagtatatcccaaa 544
QY 541 attgtagagatttcttcagatatctccattaatgaagggaacaatatattagcctcactgc 600

Db 545 attgtagagatttcttcagatatctccattaatgaagggaacaatatattagcctcactgc 604
QY 601 atagcaactgttagaccagagcctctacgttacttggagacacatctctccaaagcggtt 660
Db 605 atagcaactgttagaccagagcctctacgttacttggagacacatctctccaaagcggtt 664
QY 661 ggcttgtgtgaagacgacgaatacttggaaattcagggcattcaccgggagcagtcagg 720
Db 665 ggcttgtgtgaagacgacgaatacttggaaattcagggcattcaccgggagcagtcagg 724
QY 721 gactacgagtgacagtgctcctccaatgacgtggccgctgtgtaagagagtaaaagttc 780
Db 725 gactacgagtgacagtgctcctccaatgacgtggccgctgtgtaagagagtaaaagttc 784
QY 781 accgtgaactatccaccatacatcttcagaagccaagggtacaggtgtccccgttggacaa 840
Db 785 accgtgaactatccaccatacatcttcagaagccaagggtacaggtgtccccgttggacaa 844
QY 841 aaggggacactgacgtgtgaagcctcagcagtcctccctcagcagaattccagttgtacaa 900
Db 845 aaggggacactgacgtgtgaagcctcagcagtcctccctcagcagaattccagttgtacaa 904
QY 901 gatgacaaagacgtattgaaggaagaagaagggtgaagtggaacacagaccttcctc 960
Db 905 gatgacaaagacgtattgaaggaagaagaagggtgaagtggaacacagaccttcctc 964
QY 961 tcaaaactcatctcttcataatgtcttgaacatgactatgggaactacacttgcgtggcc 1020
Db 965 tcaaaactcatctcttcataatgtcttgaacatgactatgggaactacacttgcgtggcc 1024
QY 1021 tccaaagaagctgggcccacacccaatgccaagcatatgtatttggccaggcgctcagc 1080
Db 1025 tccaaagaagctgggcccacacccaatgccaagcatatgtatttggccaggcgctcagc 1084
QY 1081 gaggtgagcaaacgcgcgctcgaggaaggcaggtcgtctgtgctgtcctctctgtgc 1140
Db 1085 gaggtgagcaaacgcgcgctcgaggaaggcaggtcgtctgtgctgtcctctctgtgc 1144
QY 1141 ttgcacctgtctcctcaaatlttgatgtgagtgccacttcccaccgggaagggtcgcc 1200
Db 1145 ttgcacctgtctcctcaaatlttgatgtgagtgccacttcccaccgggaagggtcgcc 1204
QY 1201 ccaccacccacccacacacacagcgaatgccaacccgacagcacaaccaatcagatatata 1260
Db 1205 ccaccacccacccacacacacagcgaatgccaacccgacagcacaaccaatcagatatata 1264
QY 1261 caaatgaaattagaagaacacacagcctcatgtgacagaagaatttgaggaggggacaana 1320
Db 1265 caaatgaaattagaagaacacacagcctcatgtgacagaagaatttgaggaggggacaana 1324
QY 1321 aatacttggggggaaaaaagttttaaaaaagaagaattggaattgcttgcagatattta 1380
Db 1325 aatacttggggggaagaagttttaaaaaagaagaattggaattgcttgcagatattta 1384
QY 1381 ggtacaatgagtttcttcccaaacgggaagacacacagcaccggcttgcagacc 1440
Db 1385 ggtacaatgagtttcttcccaaacgggaagacacacagcaccggcttgcagacc 1444
QY 1441 ctgcaagctgcatcgtgcaacctcttggctgacagtgtyggcaagggtcagcctctctg 1500
Db 1445 ctgcaagctgcatcgtgcaacctcttggctgacagtgtyggcaagggtcagcctctctg 1504
QY 1501 cccacagagtgccccccacgctggaacatctctgagctggccatcccaaatccaatcagttcc 1560
Db 1505 cccacagagtgccccccacgctggaacatctctgagctggccatcccaaatccaatcagttcc 1564
QY 1561 atagagacgaacagaatgagaccttcggcccaagcgttgccgtgcggggcactttgttag 1620
Db 1565 atagagacgaacagaatgagaccttcggcccaagcgttgccgtgcggggcactttgttag 1624
QY 1621 actgtgccaccacggcgctgtgttgtgaaacgtgaaataaaaaagagcaaaaaaa 1675

Db 1625 actgtgccaccacgcgtgtgtgtgaacactgaataaagaagcaaaaaa 1679

RESULT 4

AAS21431

ID AAS21431 standard; cDNA; 1679 BP.

XX AAS21431;

AC AAS21431;

XX 24-OCT-2001 (first entry)

DE Human cDNA sequence encoding for PRO337 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

KW adipocyte; A-peptide; factor VIIa; gene therapy; ss.

XX Homo sapiens.

OS

XX WO200140466-A2.

PN

XX 07-JUN-2001.

PD

XX 01-DEC-2000; 2000WO-US32678.

PF

XX 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31243.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 10-NOV-2000; 2000WO-US30873.

XX (GETH) GENENTECH INC.

PA

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

DR P-PSDB; AAU12359.

DR

XX Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing

PT PRO polypeptides, and detect the presence of mammalian tumours e.g.

PT lung, breast, prostate, cervical

XX

PS Claim 3; Fig 375; 813pp; English.

XX

CC AAS21244-AAS21518 encode for novel human secretory and transmembrane

CC PRO polypeptides. The PRO polypeptides are useful to detect other

CC PRO polypeptides, to link bioactive molecules to cells expressing

CC PRO polypeptides, to modulate biological activities of cells expressing

CC PRO polypeptides, and to detect the presence of mammalian lung, colon,

CC breast, prostate, rectal, cervical or liver tumours by comparing PRO

CC polypeptide expression in a cell sample to that in a control sample.

CC Some of the 275 sequences are also useful to stimulate the release of

CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the

CC proliferation or differentiation of chondrocytes, the proliferation or

CC gene expression in pericyte cells, the release of proteoglycans from

CC cartilage, the proliferation of inner ear utricular supporting cells or

CC of T-lymphocytes, the release of a cytokine from peripheral blood

CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of

CC the PRO polypeptides may modulate glucose or free fatty acid uptake by

CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

CC to factor VIIA. The PRO polypeptides can be used in assays to identify

CC molecules involved in binding interactions. The polynucleotides encoding

CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,

CC transgenic or knock out animals and can be used in gene therapy.

XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 98.1%; Score 1661.4; DB 22; Length 1679;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtccctcagcaaaacagtgatlttaattccttcgcaaaagcttgagagcaacaatct 60

Db 6 gtccctcagcaaaacagtgatlttaattccttcgcaaaagcttgagagcaacaatct 65

QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120

Db 66 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 124

QY 121 aaaaaaatcgtgaaaacccatccagcccaaaatgtcacaaattctatctcttggcaatcttc 180

Db 125 aaaaaaatcgtgaaaacccatccagcccaaaatgtcacaaattctatctcttggcaatcttc 184

QY 181 acgggctgctgtctgtgtctcttccaaagagtgcccgctgcgcagcgagatgccacc 240

Db 185 acgggctgctgtgtgtctcttccaaagagtgcccgctgcgcagcgagatgccacc 244

QY 241 ttccccaagctatgtgacaacgtgacggtccggcaggaggagcgccaccctcaggtgc 300

Db 245 ttccccaagctatgtgacaacgtgacggtccggcaggaggagcgccaccctcaggtgc 304

QY 301 actatgacaacccggttcaccccggttgccctgctaaccgagcaccatctctatgtct 360

Db 305 actatgacaacccggttcaccccggttgccctgctaaccgagcaccatctctatgtct 364

QY 361 gggaatgacaagtgtgctgtgctcctcgtgtgtctcttgagcaaccaccaagcag 420

Db 365 gggaatgacaagtgtgctgtgctcctcgtgtgtctcttgagcaaccaccaagcag 424

QY 421 tacagcatcgagatccagaacgtgtgtatgtatgacgaggcccttacacctgtcgtg 480

Db 425 tacagcatcgagatccagaacgtgtgtatgtatgacgaggcccttacacctgtcgtg 484

QY 481 cagacagacaaccccaaaagaacctctagggctccacctcatgttgcaagtatctccaaa 540

Db 485 cagacagacaaccccaaaagaacctctagggctccacctcatgttgcaagtatctccaaa 544

QY 541 attgtagagatttctcagatattcattatgaaggaagaacaatatgtcctcacctgc 600

Db 545 attgtagagatttctcagatattcattatgaaggaagaacaatatgtcctcacctgc 604

QY 601 atagaactgttagaccagagccttaagcttacttgagacacatctctccaaagcgtt 660

Db 605 atagaactgttagaccagagccttaagcttacttgagacacatctctccaaagcgtt 664

QY 661 ggccttgtagtgaagcgaatatttggaattcagggcatacccgaggagcagtcaggg 720

Db 665 ggccttgtagtgaagcgaatatttggaattcagggcatacccgaggagcagtcaggg 724

QY 721 gactacgagtgagtgctctccaatgacgctggccgcgtgtgtacgagagtaaaagctc 780
|||||
Db 725 gactacgagtgagtgctctccaatgacgctggccgcgtgtgtacgagagtaaaagctc 784
QY 781 accgtgaactatccaccataatttcagaagccaaggtacagtgctcccgctgggacaa 840
|||||
Db 785 accgtgaactatccaccataatttcagaagccaaggtacagtgctcccgctgggacaa 844
QY 841 aaggggacactgagtgtagagcctcagcagctccctcagcagaattccagtggtacaag 900
|||||
Db 845 aaggggacactgagtgtagagcctcagcagctccctcagcagaattccagtggtacaag 904
QY 901 gatgacaaaagactgattgaaggaagaaggggtgaagtggaanaacagaccttcctc 960
|||||
Db 905 gatgacaaaagactgattgaaggaagaaggggtgaagtggaanaacagaccttcctc 964
QY 961 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttgctgccc 1020
|||||
Db 965 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttgctgccc 1024
QY 1021 tccaaacagctgggccaacccaatgccaacatcatgtattgttccagcgccgtcagc 1080
|||||
Db 1025 tccaaacagctgggccaacccaatgccaacatcatgtattgttccagcgccgtcagc 1084
QY 1081 gagtgagcaacggaacgctcgaggaaggcgagctgctgctgctgctctctctgtc 1140
|||||
Db 1085 gagtgagcaacggaacgctcgaggaaggcgagctgctgctgctgctctctctgtc 1144
QY 1141 ttgcacctgcttccaattttgtatgtgagtgccacttcccaaccgggaaaggtgccg 1200
|||||
Db 1145 ttgcacctgcttccaattttgtatgtgagtgccacttcccaaccgggaaaggtgccg 1204
QY 1201 ccaccaccaccaccacacacacagcaatgccaaccgacagcaaccaatcagatatata 1260
|||||
Db 1205 ccaccaccaccaccacacacacagcaatgccaaccgacagcaaccaatcagatatata 1264
QY 1261 caaatgaaattagaagaacacacagcctcatgaggacagaatttgaggaggggaacaaag 1320
|||||
Db 1265 caaatgaaattagaagaacacacagcctcatgaggacagaatttgaggaggggaacaaag 1324
QY 1321 aatacttgggggaaaaaagtlttaaaaaaagaattgaaattgccttgcagatatatta 1380
|||||
Db 1325 aatacttgggggaaaaaagtlttaaaaaaagaattgaaattgccttgcagatatatta 1384
QY 1381 ggtacaatggagtttcttcttcccaaacgggaagaacacagcacaccggtctggaacca 1440
|||||
Db 1385 ggtacaatggagtttcttcttcccaaacgggaagaacacagcacaccggtctggaacca 1444
QY 1441 ctgcaagctgcatcgtgcaacctctttgtgtgccaagtgtggcgaagggtcagcctctctg 1500
|||||
Db 1445 ctgcaagctgcatcgtgcaacctctttgtgtgccaagtgtggcgaagggtcagcctctctg 1504
QY 1501 cccacagagtgcccccacgtggaacattctgagctggccaatcccaaatccaatcagctcc 1560
|||||
Db 1505 cccacagagtgcccccacgtggaacattctgagctggccaatcccaaatccaatcagctcc 1564
QY 1561 atagagaagaaacagaatgagaccttccggcccaagcgtggcctggcggaactttgtag 1620
|||||
Db 1565 atagagaagaaacagaatgagaccttccggcccaagcgtggcctggcggaactttgtag 1624
QY 1621 actgtgccaccacagcgctgtgtgtgtgtaaaacgtgtaataaaaaagagcaaaaaaaa 1675
|||||
Db 1625 actgtgccaccacagcgctgtgtgtgtgtaaaacgtgtaataaaaaagagcaaaaaaaa 1679

RESULT 5
AAC87037
ID AAC87037 standard; cDNA: 1679 BP.
XX AAC87037;
AC
XX
DT 20-APR-2001 (first entry)
XX

DE Nucleotide sequence of human polypeptide PRO337.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO183; PRO1272; PRO1419; PRO499; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
SS.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 134..1168
FT sig_peptide /*tag= a 134..216
FT /*tag= b
PN WO200077037-A2.
XX
PD 21-DEC-2000.
XX
PF 22-MAY-2000; 2000WO-US14042.
XX
PR 15-JUN-1999; 99US-0139695.
PR 20-JUL-1999; 99US-0145070.
PR 26-JUL-1999; 99US-0145698.
PR 17-AUG-1999; 99US-0149396.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 07-DEC-1999; 99US-0169495.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrera N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
DR P-PSDB; AAB31204.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
XX
PS Claim 2; Fig 51; 244pp; English.
XX
CC The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO183, PRO1272, PRO1419, PRO499, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these

CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene.

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 98.1%; Score 1661.4; DB 22; Length 1679;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtccttcagcaaacagtgatttaattctccttcagcaagcttgagagcaacaatct 60
 |||||
 Db 6 gtccttcagcaaacagtgatttaattctccttcagcaagcttgagagcaacaatct 65
 QY 61 atcaggaagaagaagaaaaaacggaacctgacaaaagaagaagaagaaga 120
 |||||
 Db 66 atcaggaagaagaagaaag-aaaaaacggaacctgacaaaagaagaagaagaaga 124
 QY 121 aaaaaaatcatgaataaacatccagccaaaatgacaaattctatctcttggaatcttc 180
 |||||
 Db 125 aaaaaaatcatgaataaacatccagccaaaatgacaaattctatctcttggaatcttc 184
 QY 181 acggggtgctgtctgtctgtctcttccaaaggagtgccgtgagcgagatgcccacc 240
 |||||
 Db 185 acggggtgctgtctgtctgtctcttccaaaggagtgccgtgagcgagatgcccacc 244
 QY 241 ttccccaagaagctatgagcaacgctgacggtccggcaggaggagagccaccctcaggtgc 300
 |||||
 Db 245 ttccccaagaagctatgagcaacgctgacggtccggcaggaggagagccaccctcaggtgc 304
 QY 301 actatgcaaacgggtcaccgggtgctgctggtctaaaccgagaccatctctatgtct 360
 |||||
 Db 305 actatgcaaacgggtcaccgggtgctgctggtctaaaccgagaccatctctatgtct 364
 QY 361 gggaatgacaagtgtgctgtgctgctcgtgtgtctctctgagcaacccaacgag 420
 |||||
 Db 365 gggaatgacaagtgtgctgtgctgctcgtgtgtctctctgagcaacccaacgag 424
 QY 421 taccgcatcgagatccagaaagtgatgtatgacgaggcccttacacctgtcgtg 480
 |||||
 Db 425 taccgcatcgagatccagaaagtgatgtatgacgaggcccttacacctgtcgtg 484
 QY 481 cagacagacaacccaacaaagcctctaagggtccacctcatgtgcaagtatactcccaaa 540
 |||||
 Db 485 cagacagacaacccaacaaagcctctaagggtccacctcatgtgcaagtatactcccaaa 544
 QY 541 attgtagagattcttcagatatctccatgaatgaaggagacaatatgacctcagctgc 600
 |||||
 Db 545 attgtagagattcttcagatatctccatgaatgaaggagacaatatgacctcagctgc 604
 QY 601 atagcaactgttagaccagagcctagcttacttgagacacatctctcccaagcggt 660
 |||||
 Db 605 atagcaactgttagaccagagcctagcttacttgagacacatctctcccaagcggt 664
 QY 661 ggcttgtgagtgaagacgaataacttggaatcagggcatcaccgggagcagtcaggg 720
 |||||
 Db 665 ggcttgtgagtgaagacgaataacttggaatcagggcatcaccgggagcagtcaggg 724
 QY 721 gactacgagtgcaagtgccctccaatgacgtgcccgcgctgtgtaagagagtaaggtc 780
 |||||
 Db 725 gactacgagtgcaagtgccctccaatgacgtgcccgcgctgtgtaagagagtaaggtc 784
 QY 781 accgtgaactatccacatacatctcagaagccaaggtgtacaggtgtcccccgtggagcaa 840
 |||||
 Db 785 accgtgaactatccacatacatctcagaagccaaggtgtacaggtgtcccccgtggagcaa 844
 QY 841 aaggagcaactgcagtgtagcgcctcagcagctccctcagcagaattccagtggtacaag 900
 |||||

Db 845 aaggggacactgcagtgtagaagcctcagcagctccctcagcagcaaatccagtggtacaag 904
 QY 901 gatgacaacaaagactgattgaaggaagaagggtgtaaaagtgaacagaccttctc 960
 |||||
 Db 905 gatgacaacaaagactgattgaaggaagaagggtgtaaaagtgaacagaccttctc 964
 QY 961 tcaaaactcatctcttccaatgtctctgaacatgactatggaactacactgctggtgc 1020
 |||||
 Db 965 tcaaaactcatctcttccaatgtctctgaacatgactatggaactacactgctggtgc 1024
 QY 1021 tccaacaagctggtgccaacaaatgccaagcatatgtctatttgtccaggcgccgtcagc 1080
 |||||
 Db 1025 tccaacaagctggtgccaacaaatgccaagcatatgtctatttgtccaggcgccgtcagc 1084
 QY 1081 gaggtgagcaacgagcagctcgagagaggcaggtgctgctgctgctctctgtc 1140
 |||||
 Db 1085 gaggtgagcaacgagcagctcgagagaggcaggtgctgctgctgctctctgtc 1144
 QY 1141 ttgacctgtcttccaatttggatgtgagtgccacttccccaacggggaaggtgcg 1200
 |||||
 Db 1145 ttgacctgtcttccaatttggatgtgagtgccacttccccaacggggaaggtgcg 1204
 QY 1201 ccaccaccaaccaaccaacacagcagcaatgccaacacgacagcaaccaatcagatatata 1260
 |||||
 Db 1205 ccaccaccaaccaaccaacacagcagcaatgccaacacgacagcaaccaatcagatatata 1264
 QY 1261 caaatgaaattagaagaacaacacagcctcatctggtgagagaatlttgaggagggaacaag 1320
 |||||
 Db 1265 caaatgaaattagaagaacaacacagcctcatctggtgagagaatlttgaggagggaacaag 1324
 QY 1321 aatacttggggggaagaaagtttaaaaaagaagaatltgaaattgaccttgagatatlla 1380
 |||||
 Db 1325 aatacttggggggaagaaagtttaaaaaagaagaatltgaaattgaccttgagatatlla 1384
 QY 1381 ggtacaatgagtttcttcttcccaaacgggaagaacacagcacaccggcttgagccca 1440
 |||||
 Db 1385 ggtacaatgagtttcttcttcccaaacgggaagaacacagcacaccggcttgagccca 1444
 QY 1441 ctgcaagctgcacgtgcaacaccttctgtggtccaggtgtggtgcaaggtctcagctctctg 1500
 |||||
 Db 1445 ctgcaagctgcacgtgcaacaccttctgtggtccaggtgtggtgcaaggtctcagctctctg 1504
 QY 1501 cccaagagatgccccccacgctggaacatcttgagctggtgcatcccaatccaatcagtc 1560
 |||||
 Db 1505 cccaagagatgccccccacgctggaacatcttgagctggtgcatcccaatccaatcagtc 1564
 QY 1561 atagagaagcaagaatgagacaccttcggcccaagcgtggtggtggtggtggtgag 1620
 |||||
 Db 1565 atagagaagcaagaatgagacaccttcggcccaagcgtggtggtggtggtggtgag 1624
 QY 1621 actgtgccaccacggcggtgtgtgtgtgtaaacgtgtaataaaagagcaaaaaaaa 1675
 |||||
 Db 1625 actgtgccaccacggcggtgtgtgtgtgtaaacgtgtaataaaagagcaaaaaaaa 1679
 |||||

RESULT 6

AAA88791 ID AAA88791 standard; cDNA; 2012 BP.

AC AAA88791;

DT 19-FEB-2001 (first entry)

DE Human SECX cDNA Clone 11753149.0.37.

XX SECX; human; diagnosis; gene therapy; cell adhesion; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 501..1535

FT sig_peptide 501..599

FT /*tag= b
FT mat_peptide 600..1532
FT /*tag= c
XX NO200061754-A2.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-US09392.
XX 09-APR-1999; 99US-0128514.
XX 03-MAR-2000; 2000US-0128514.
XX (CURA-) CURAGEN CORP.
XX Fernandez E, Vernet C, Shinkets R;
XX WPI; 2000-679487/66.
XX P-PSDB; AABI9722.

PT SECX polypeptides and the nucleic acids that encode them, useful for
PT diagnosing, preventing and treating e.g. cancers,. inflammation,
PT arthritis and immunological disorders -
XX
XX Claim 14; Fig 3; 143pp; English.

XX The present sequence is that of SECX Clone 11753149.0.37, which
CC resembles rat neural cell adhesion molecule neurotrimin and human
CC opioid binding protein/cell adhesion molecule OBCAM. The clone
CC was initially identified in human foetal brain tissue. The
CC invention provides novel SECX polynucleotides (see AAA88789-804) and
CC the secreted or membrane-associated proteins encoded by them
CC (see AABI9720-34). SECX polynucleotides, polypeptides and antibodies
CC can be used in the detection, diagnosis and treatment (including
CC gene therapy) of a broad range of pathological states.
XX
XX Sequence 2012 BP; 567 A; 503 C; 512 G; 430 T; 0 other;

Query Match 96.0%; Score 1625.8; DB 21; Length 2012;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 gtccttcagcaaaacagtgatttaaatctccttcgacaagcttgagagcaacaaatct 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 373 gtccttcagcaaaacagtgatttaaatctccttcgacaagcttgagagcaacaaatct 432
QY 61 atcagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 433 atcagaaagaaagaaag-aaaaaacgcgaacctgacaaaaaagaaagaaagaaagaa 491
QY 121 aaaaaatcatgaaacatccacagccaaaatgacaaattctatctcttggcaatctc 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 492 aaaaaatcatgaaacatccacagccaaaatgacaaattctatctcttggcaatctc 551
QY 181 acggggtgctgtctgtctcttccaaggagtgcccgtygcagcggagatgcacc 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 552 acggggtgctgtctgtctcttccaaggagtgcccgtygcagcggagatgcacc 611
QY 241 tcccccaagctatgacaaagtgaacgtccgcaggggagagcgccaccctcagtygc 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 612 tcccccaagctatgacaaagtgaacgtccgcaggggagagcgccaccctcagtygc 671
QY 301 actattgacaacccgggtcaaccgggtgctgcttaaacccgcagcacatcctatgct 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 672 actattgacaacccgggtcaaccgggtgctgcttaaacccgcagcacatcctatgct 731
QY 361 gggaatgacaagtgtgcttgatcctcggtgtgtccttctgagcaacccccaaacgag 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 732 gggaatgacaagtgtgcttgatcctcggtgtgtccttctgagcaacccccaaacgag 791
QY 421 tacagcatcgagatccagaacgtgtatgtatgacagagggcccttacacctgtcgtg 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 792 tacagcatcgagatccagaacgtgtatgtatgacagagggcccttacacctgtcgtg 851
QY 481 cagacagacaacccccaaagacctctaggggtccacctaatgttgcaagratctcccaa 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 852 cagacagacaacccccaaagacctctaggggtccacctaatgttgcaagratctcccaa 911
QY 541 attgtagagattcttcagatatctccaatgaagggaaacaatatagcctcacctgc 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 912 attgtagagattcttcagatatctccaatgaagggaaacaatatagcctcacctgc 971
QY 601 atagcaactgtgtagaccagagcctacggttacttgtagacacatctctccaaagcggt 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 972 atagcaactgtgtagaccagagcctacggttacttgtagacacatctctccaaagcggt 1031
QY 661 ggccttgtgagtgaagcgaatacttgaataatcagggcatacccgggagcagtcagg 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1032 ggccttgtgagtgaagcgaatacttgaataatcagggcatacccgggagcagtcagg 1091
QY 721 gactacgagtgacagtcctccaatgacgtgcccgcgcccgtgtgacggagtaaggtc 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1092 gactacgagtgacagtcctccaatgacgtgcccgcgcccgtgtgacggagtaaggtc 1151
QY 781 accgtgaactatccacacatacatctcagaagccaaagggtacaggtgtcccggtggacaa 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1152 accgtgaactatccacacatacatctcagaagccaaagggtacaggtgtcccggtggacaa 1211
QY 841 aaggggacactgcagctgtgaagcctcagcagtcctccctcagcagaattccagtggtacaag 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1212 aaggggacactgcagctgtgaagcctcagcagtcctccctcagcagaattccagtggtacaag 1271
QY 901 gatgcaaaaagactgatgtgaagaaagaaagggtgaaggtggaagaaacagaccttcctc 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1272 gatgcaaaaagactgatgtgaagaaagaaagggtgaaggtggaagaaacagaccttcctc 1331
QY 961 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttgcgtggcc 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1332 tcaaaactcatcttcttcaatgtctctgaacatgactatggaactacacttgcgtggcc 1391
QY 1021 tccaacaagctgggccaacacccaatgccaagcatcatgtctattgttccaggcgccgtcagc 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1392 tccaacaagctgggccaacacccaatgccaagcatcatgtctattgttccaggcgccgtcagc 1451
QY 1081 gaggtgagcaacgycagcgtcgagagggcagggcgtcgtcgtcgtcctctctgtgc 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1452 gaggtgagcaacgycagcgtcgagagggcagggcgtcgtcgtcgtcctctctgtgc 1511
QY 1141 ttgcacctgtcttcaaatlttgatgtgagtgccactcccccggggaaagcgtgcg 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1512 ttgcacctgtcttcaaatlttgatgtgagtgccactcccccggggaaagcgtgcg 1571
QY 1201 ccaccacccaaccaaccaacagcagatgccaacccgcagcagcaaccaatcagatatata 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1572 ccaccacccaaccaaccaacagcagatgccaacccgcagcagcaaccaatcagatatata 1631
QY 1261 caaatgaaattagaagaacacacagcctcatggtgacagaaatttgagggagggaacaag 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1632 caaatgaaattagaagaacacacagcctcatggtgacagaaatttgagggagggaacaag 1691
QY 1321 aatacttggggggaaaaaagltttaaanaagaatatgaaattgacctgagatatita 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1692 aatacttggggggaaaaaagltttaaanaagaatatgaaattgacctgagatatita 1751
QY 1381 ggtacaatgaglttcttcttccaaacggggaagaacacagcacaccggcttgagacca 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1752 ggtacaatgaglttcttcttccaaacggggaagaacacagcacaccggcttgagacca 1811
QY 1441 ctgcaagctgcatcgttgcaacctcttggtyccagtgtyggcaagggtcagcctctctg 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1812 ctgcaagctgcatcgttgcaacctcttggtyccagtgtyggcaagggtcagcctctctg 1871
QY 1501 cccacagagtgccccccacgtyggaacatctcgtgagctggtccatcccaaatcactcagtc 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1872 cccacagagtgccccccacgtyggaacatctcgtgagctggtccatcccaaatcactcagtc 1931

QY	1178	tccccaccccggaagcgtgcgcccaccaccaccaccaacaagaatgycaacacc	1237
Dd	1140	tccccaccccggaagcgtgcgcccaccaccaccaccaacaagaatgycaacacc	1199
QY	1238	gcacgcaaccaatcatgatataataatgaaattagaagaaaacacagctcatyggacag	1297
Dd	1200	gcacgcaaccaatcatgatataataatgaaattagaagaaaacacagctcatyggacag	1259
QY	1298	aactttgaggagggggaacaaagaatacttggggggaaaaaagtlttaaaaaaat	1357
Dd	1260	aaatttgaggagggggaacaaagaatacttggggggaaaaaagtlttaaaaaaat	1319
QY	1358	gaaaatctgccttcgcagatatattaggtacaatgtagtttcttcccaaacygaagAAC	1417
Dd	1320	gaaaatctgccttcgcagatatattaggtacaatgtagtttcttcccaaacygaagAAC	1379
QY	1418	acacgacacacccgcgtttggaccceactgcagctgcacgttgtcaaccttctgcgccactgtg	1477
Dd	1380	acacgacacacccgcgtttggaccceactgcagctgcacgttgtcaaccttctgtgccactgtg	1439
QY	1478	tggcgcaagggtctcagcctctctgcgccacagagtgcgccccaagtggaaatctctgagctg	1537
Dd	1440	tggcgcaagggtctcagcctctctgcgccacagagtgcgccccaagtggaaatctctgagctg	1499
QY	1538	gccatccccaatcataatcatgcataagagacgaacagaatggaaccttcgcgcccacagcg	1597
Dd	1500	gccatccccaatcataatcatgcataagagacgaacagaatggaaccttcgcgcccacagcg	1559
QY	1598	tggcgctgcgggcactttgttagactgtgccaccacgcygctgtg	1641
Dd	1560	tggcgctgcgggcactttgttagactgtgccaccacgcygctgtg	1603

RESULT	ID	AAI57869	standard; cdNA; 1678 BP.
XX	AC	AAI57869;	
XX	DI	22-OCT-2001	(first entry)
XX	DE	Human polynucleotide SEQ	ID NO 72.
XX	KW	Human; nootropic; immunosuppressant; cyrostatic; gene therapy; cancer;	
KW	KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
XX	OS	leukaemia; ss.	
XX	PN	Homo sapiens.	
XX	PD	WO200153312-A1.	
XX	PF	26-JUL-2001.	
XX	PR	26-DEC-2000; 2000WO-US34263.	
XX	PR	21-JAN-2000; 2000US-0488725.	
XX	PR	25-APR-2000; 2000US-0552317.	
XX	PR	09-JUL-2000; 2000US-0598042.	
XX	PR	19-JUL-2000; 2000US-0620312.	
XX	PR	03-AUG-2000; 2000US-0653450.	
XX	PR	14-SEP-2000; 2000US-0662191.	
XX	PR	19-OCT-2000; 2000US-0693036.	
XX	PR	29-NOV-2000; 2000US-0727344.	
XX	PA	(HYSE-) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,	
XX	PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
XX	PI	Zhao QA, Zhou P, Goodlich R, Drmanac RT;	

XX WPI; 2001-442253/47.
DR P-PSDB; AAM38713.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 72; 10078pp; English.

AA The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

Sequence 1678 BP; 420 A; 468 C; 451 G; 339 T; 0 other;

Query Match	86.0%;	Score 1455.4;	DB 22;	Length 1678;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1456; Conservative	0;	Mismatches	1;	Indels 0;
		Gaps		0;

QY	210	aggagttgcccgctgcgcagcgcgagatgtccaccttccccaagctatgtgaacaacgctaacggt	269
Db	222	aggagttgcccgctgcgcagcgcgagatgtccaccttccccaagctatgtgaacaacgctaacggt	281
QY	270	ccgcgcagggggagagcgcgccacctcaggtgtcactatgtgaacaaccggttcacccgggtggc	329
Db	282	ccgcgcagggggagagcgcgccacctcaggtgtcactatgtgaacaaccggttcacccgggtggc	341
QY	330	ctgtgctaaaccgcagcacccatcctcttctgtgtggaatgtacaagtgtgtgtcctgtgattcctcg	389
Db	342	ctgtgctaaaccgcagcacccatcctcttctgtgtggaatgtacaagtgtgtgtcctgtgattcctcg	401
QY	390	cgtgtgtccttctgtagccaacccaacacgcagtlacagacatcagatccagaacgctgtgatgt	449
Db	402	cgtgtgtccttctgtagccaacccaacacgcagtlacagacatcagatccagaacgctgtgatgt	461
QY	450	gtatgacgaggggccccttacacctgtcgtcgtgtgcagacagacaaccaccaagacctctag	509
Db	462	gtatgacgaggggccccttacacctgtcgtcgtgtgcagacagacaaccaccaagacctctag	521
QY	510	gttcaccctcatattgtgcagaatatctcccaaaattgttagagatttcttcagatatctccat	569
Db	522	gttcaccctcatattgtgcagaatatctcccaaaattgttagagatttcttcagatatctccat	581
QY	570	taatgaagggaaacaatatatgaagcctcacacctgtcatagcaactgtgtagaccaagcctaacggt	629
Db	582	taatgaagggaaacaatatatgaagcctcacacctgtcatagcaactgtgtagaccaagcctaacggt	641
QY	630	tacttggagacacatctctcccaagcggltgtgcttltgtgagtgaagacgnaatacttgya	689
Db	642	tacttggagacacatctctcccaagcggltgtgcttltgtgagtgaagacgnaatacttgya	701
QY	690	aattcagggcatcacccgggagcagtlcaggggactacagatgtcagtlgtccccaatgacgt	749
Db	702	aattcagggcatcacccgggagcagtlcaggggactacagatgtcagtlgtccccaatgacgt	761
QY	750	ggccgcgcgccgtgtgtacggagagtaaaaggtcacccgtgaactataccaccatacatttcaga	809
Db	762	ggccgcgcgccgtgtgtacggagagtaaaaggtcacccgtgaactataccaccatacatttcaga	821

QY 810 agccaagggtacaggtgtcccccgtggtgacaaaagggtgacactgcagtgtgaagcctcagc 869
Db 822 agccaagggtacaggtgtcccccgtggtgacaaaagggtgacactgcagtgtgaagcctcagc 881
QY 870 agtccctcagcagaattccaggtgtacaaagatgacaaaagactgtatgaagaaagaa 929
Db 882 agtccctcagcagaattccaggtgtacaaagatgacaaaagactgtatgaagaaagaa 941
QY 930 aggggtgaagtggaaaaacagacccttctctcaaaactcatcttctcaatgtctctga 989
Db 942 aggggtgaagtggaaaaacagacccttctctcaaaactcatcttctcaatgtctctga 1001
QY 990 acatgactatgggaaactacacttgcgtggtcctccaagaagctgggccacccaatggcag 1049
Db 1002 acatgactatgggaaactacacttgcgtggtcctccaagaagctgggccacccaatggcag 1061
QY 1050 catcatgtctatttgcgtccagggccgttcagcggaggtgaagaaacggcacgtcgaggagcg 1109
Db 1062 catcatgtctatttgcgtccagggccgttcagcggaggtgaagaaacggcacgtcgaggagcg 1121
QY 1110 aggcgtcgtctgctgtgctctctctgtgtctgacactgtcttcaaatctgagtga 1169
Db 1122 aggcgtcgtctgctgtgctctctctgtgtgtgacactgtcttcaaatctgagtga 1181
QY 1170 gtgccacttccccccggggaaggtgtccgcgccaccaccacccaacacacagcaatg 1229
Db 1182 gtgccacttccccccggggaaggtgtccgcgccaccaccacccaacacacagcaatg 1241
QY 1230 gcaacaccgacagcaaccaatcagatatatacaaatgaaatttagaagaacacagcctca 1289
Db 1242 gcaacaccgacagcaaccaatcagatatatacaaatgaaatttagaagaacacagcctca 1301
QY 1290 tgggacagaaatttgaaggaggggaacaaagaatacttgggggggaaagtttaaaa 1349
Db 1302 tgggacagaaatttgaaggaggggaacaaagaatacttgggggggaaagtttaaaa 1361
QY 1350 aagaataatgaaattgccttgcaagatatattgagtlacaatgaggttcttcccaacg 1409
Db 1362 aagaataatgaaattgccttgcaagatatattgagtlacaatgaggttcttcccaacg 1421
QY 1410 ggaagaacacagcaaccggccttggaccactgcaagctgcacgtgcgaacctcttgg 1469
Db 1422 ggaagaacacagcaaccggccttggaccactgcaagctgcacgtgcgaacctcttgg 1481
QY 1470 tgcaggtgtggcaagggtcagcctctctgcccacagagtgccccacgttgaacatc 1529
Db 1482 tgcaggtgtggcaagggtcagcctctctgcccacagagtgccccacgttgaacatc 1541
QY 1530 tggagctggccatcccaaatcattcattcattagagacgacagaatgagaccttcgg 1589
Db 1542 tggagctggccatcccaaatcattcattcattagagacgacagaatgagaccttcgg 1601
QY 1590 cccaagcgtggcgtcggggcaacttggtagactgtgccaccacggcgtgtgtgtgaaa 1649
Db 1602 cccaagcgtggcgtcggggcaacttggtagactgtgccaccacggcgtgtgtgtgaaa 1661
QY 1650 cgtgaaataaaaagagc 1666
Db 1662 cgtgaaataaaaagagc 1678

RESULT 9
AA159655
ID AA159655 standard; cDNA; 1690 BP.
XX AA159655;
AC
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 3644.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
OS
XX Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM40499.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 3644; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 1690 BP; 482 A; 416 C; 425 G; 367 T; 0 other;

Query Match 76.6%; Score 1297.4; DB 22; Length 1690;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1342; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 1 gtccctcagcaaacagtgatttaattcctcttgcaacaagcttgagagcacacaatct 60
Db 346 gtccctcagcaaacagtgatttaattcctcttgcaacaagcttgagagcacacaatct 405
QY 61 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 120
Db 406 atcaggaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 464
QY 121 aaaaaaatcatgaaaccatccagccaaaatgcaaatctatctcttggcaatctc 180
Db 465 aaaaaaatcatgaaaccatccagccaaaatgcaaatctatctcttggcaatctc 524
QY 181 acggggctgtgtctgtctctctccaagagtgcccggtgcgacggagatgccacc 240

Db 525 acgggctgctgtctgtctgtcttccaaagagtgcccgctgcgacgagagatgcccacc 584
 QY 241 ttcccaaaagctatggaacaacgttaacggtcccgacaggggagagcgccaccctcagtg 300
 Db 585 ttcccaaaagctatggaacaacgttaacggtcccgacaggggagagcgccaccctcagtg 644
 QY 301 actatgacaacccgggtcaccgggttgccctgctaaccgcagcaccatcctctatgct 360
 Db 645 actatgacaacccgggtcaccgggttgccctgctaaccgcagcaccatcctctatgct 704
 QY 361 gggaatgacaagtgtgctgctgacccctcgctgtctctctgagcaacaccccaaacgag 420
 Db 705 gggaatgacaagtgtgctgctgacccctcgctgtctctctgagcaacaccccaaacgag 764
 QY 421 tacagcatcgagatccagaacgtgatagtatgacgagggcccttacacctgctcggtg 480
 Db 765 tacagcatcgagatccagaacgtgatagtatgacgagggcccttacacctgctcggtg 824
 QY 481 cagacagacaaccccaaacgacctatagggtccacctatgtgcaagtatctcccaaa 540
 Db 825 cagacagacaaccccaaacgacctatagggtccacctatgtgcaagtatctcccaaa 884
 QY 541 attgtagagatttcttcagatatctccatataatgaagggaacatatagccctcactg 600
 Db 885 attgtagagatttcttcagatatctccatataatgaagggaacatatagccctcactg 944
 QY 601 atagcaactggttagaccagagcctaaggttacttgagacacatctctcccaagcggtt 660
 Db 945 atagcaactggttagaccagagcctaaggttacttgagacacatctctcccaagcggtt 1004
 QY 661 ggcttgtgagtgaaagcgaataacttggaaattcaggggcatcaccgggagagcagtcagg 720
 Db 1005 ggcttgtgagtgaaagcgaataacttggaaattcaggggcatcaccgggagagcagtcagg 1064
 QY 721 gactacgagtgcagtgctcctcaatgacgt-ggcccgcgccgt-ggtacggaagtaaaag 778
 Db 1065 gactacgagtgcagtgctcctcaatgacgtgagccgcgccgtggtacggaagtaaaag 1124
 QY 779 tcaccgtgaactatccaccatatacttcagaagccaagggtacaggtgtcccggtggac 838
 Db 1125 tcaccgtgaactatccaccatatacttcagaagccaagggtacaggtgtcccggtggac 1184
 QY 839 aaaaggggacactgcaagtgtgaaagcctcagcagtcctccctcagcagaatttccagtgtaca 898
 Db 1185 aaaaggggacactgcaagtgtgaaagcctcagcagtcctccctcagcagaatttccagtgtaca 1244
 QY 899 aggatgacaacgaactgattgaagaaagaaaggggtgaagtgaaagaaacagacctttcc 958
 Db 1245 aggatgacaacgaactgattgaagaaagaaaggggtgaagtgaaagaaacagacctttcc 1303
 QY 959 tctcaaaactcatcttctcaaatgtctctgaacatactatggaactacactgctgtg 1018
 Db 1304 tctcaaaactcatcttctcaaatgtctctgaacatactatggaactacactgctgtg 1363
 QY 1019 cctccaacagctgggcacacccaatgccaagcatcatgtattgttcaggcgccgtca 1078
 Db 1364 cctccaacagctgggcacacccaatgccaagcatcatgtattgttcaggcgccgtca 1423
 QY 1079 gcgaggtgagcaacgcaagctcgagggggcagcgctgctgctgctgctctcttg 1138
 Db 1424 gcgaggtgagcaacgcaagctcgagggggcagcgctgctgctgctgctctcttg 1483
 QY 1139 tcttgacctgtcttcaaatgttgatgtgagtgccaacttcccccacgggaaaggtgc 1198
 Db 1484 tcttgacctgtcttcaaatgttgatgtgagtgccaacttcccccacgggaaaggtgc 1543
 QY 1199 cgcacaccacacacacacacacagcaatggaacacccgacagcaacacacacagatata 1258
 Db 1544 cgcacaccacacacacacacacagcaatggaacacccgacagcaacacacacagatata 1603
 QY 1259 tacaatgaattagaagaaacacagcctcatggtgacagaatltgagggaggggaaaca 1318
 Db 1318 tacaatgaattagaagaaacacagcctcatggtgacagaatltgagggaggggaaaca 1318

Db 1604 tacaatgaattagaagaaacacagcctcatggtgacagaatltgagggaggggaaaca 1663
 QY 1319 agaatacttgggggggaaaaagttt 1345
 Db 1664 agaatacttgggggggaaaaagttt 1690

RESULT 10
 AAZ47892
 ID AAZ47892 standard; cDNA; 1032 BP.
 XX
 AC AAZ47892;
 XX
 DT 10-MAR-2000 (first entry)
 XX
 DE Human protein encoding cDNA SEQ ID NO:2.
 XX
 KW Human; haematopoietic cell regulation; tissue generation; reparation;
 KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
 KW receptor; ligand; autoimmune; infection-related immunodeficiency;
 KW inflammatory disorder; neurological disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1032
 FT /*tag= a
 FT /note= "no stop codon given"
 XX
 PN WO9558668-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-JP02485.
 XX
 PR 14-MAY-1998; 98JP-0131815.
 XX
 PA (ONOR) ONO PHARM CO LTD.
 XX
 PI Fukushima D, Shibayama S, Tada H;
 XX
 DR WPI; 2000-062298/05.
 DR P-PSDB; AY57601.
 DR
 XX
 PT New polypeptides of human origin having cell regulatory, tissue
 PT generation, coagulant and other activities -
 XX
 PS Claim 4; Page 41; 84pp; Japanese.
 XX
 CC The present sequence encodes a specifically claimed novel human protein.
 CC The novel human protein can be used in therapeutic drugs for the
 CC prevention and treatment of a broad range of disorders including
 CC autoimmune and infection-related immunodeficiency, inflammatory
 CC disorders, and neurological diseases. The novel protein is expected of
 CC having haematopoietic cell regulatory activity, tissue generation/
 CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
 CC blood coagulation and thrombus activity, and receptor/ligand activity.
 CC
 XX
 SQ Sequence 1032 BP; 267 A; 281 C; 270 G; 214 T; 0 other;
 Query Match 61.0%; Score 1032; DB 21; Length 1032;
 Best Local Similarity 100.0%; Pred. No. 5.6e-250;
 Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 atgaacacatccagcaaaaatgcaaatctatctcttggaacatctcaagggtg 189
 Db 1 atgaacacatccagcaaaaatgcaaatctatctcttggaacatctcaagggtg 60
 QY 190 gctgctctgtctctccaaagagtgcccggtgagcagcgagagatgcaacctcccca 249
 Db 61 gctgctctgtctctccaaagagtgcccggtgagcagcgagagatgcaacctcccca 120

QY	250	gcatatgacaacgltgacggtccggcaggggagagcgccaccctcaggtgcactatgac	309
Db	121	gcatatgacaacgltgacggtccggcaggggagagcgccaccctcaggtgcactatgac	180
QY	310	aaccgggtcacccgggtggtcgtgctaaccggcagcaccaatcctctatgctggaatgac	369
Db	181	aaccgggtcacccgggtggtcgtgctaaccggcagcaccaatcctctatgctggaatgac	240
QY	370	aagtgtgtccctggatccctcggtgtgtcctctctgagcaacacccaacgcagtacagcacc	429
Db	241	aagtgtgtccctggatccctcggtgtgtcctctctgagcaacacccaacgcagtacagcacc	300
QY	430	gagatccagaaagttgatatgttatgacgagggcccttacacctgtcgtgtcagacagac	489
Db	301	gagatccagaaagttgatatgttatgacgagggcccttacacctgtcgtgtcagacagac	360
QY	490	aaccaccccaaaagacctctagggtccacctcatttgtgcaaglatctcccaaaattgtagag	549
Db	361	aaccaccccaaaagacctctagggtccacctcatttgtgcaaglatctcccaaaattgtagag	420
QY	550	attcttcagatatctccattaatgtaaagggaacaatatatgaacctcaccgtcagacaaact	609
Db	421	attcttcagatatctccattaatgtaaagggaacaatatatgaacctcaccgtcagacaaact	480
QY	610	ggtagaccagagcgtacggttaactttgagagacacatctctccaaagcgggttgcttgg	669
Db	481	ggtagaccagagcgtacggttaactttgagagacacatctctccaaagcgggttgcttgg	540
QY	670	agtgaaagacgaataacttggaaattcagggcacatccaccggagcagtcaggggactacgag	729
Db	541	agtgaaagacgaataacttggaaattcagggcacatccaccggagcagtcaggggactacgag	600
QY	730	tgcagtgctctccaatgacgttgcgcgcgcgcgtgtgtacgagagagtaaaagttcacccgtgaac	789
Db	601	tgcagtgctctccaatgacgttgcgcgcgcgcgtgtgtacgagagagtaaaagttcacccgtgaac	660
QY	790	tatccaccatacatttcagaagccaaagggtacaggtgtccccgttggacaaaaggagaca	849
Db	661	tatccaccatacatttcagaagccaaagggtacaggtgtccccgttggacaaaaggagaca	720
QY	850	ctgcagtgtagaagcctcagcagtcctccctcagcagaattccaagtgtgtacaaagatgacaaa	909
Db	721	ctgcagtgtagaagcctcagcagtcctccctcagcagaattccaagtgtgtacaaagatgacaaa	780
QY	910	agactgatttgaaggaaagaagggttgaagttggaacaacagacotttccctcctcaaacctc	969
Db	781	agactgatttgaaggaaagaagggttgaagttggaacaacagacotttccctcctcaaacctc	840
QY	970	atctcttcaatgtctctctgaacaatgactatggtgaactacacattgctgtgcctccaacaag	1029
Db	841	atctcttcaatgtctctctgaacaatgactatggtgaactacacattgctgtgcctccaacaag	900
QY	1030	ctgggccaacacccaatgccaagcatcatgtctatttgttccaggcgccgttcagcgaggtgagc	1089
Db	901	ctgggccaacacccaatgccaagcatcatgtctatttgttccaggcgccgttcagcgaggtgagc	960
QY	1090	aacggcagctcgagagaggcgacgctgcgtctgcgtctgcctctctgtgtcttgcaacctg	1149
Db	961	aacggcagctcgagagaggcgacgctgcgtctgcgtctgcctctctgtgtcttgcaacctg	1020
QY	1150	cttctccaattt 1161	
Db	1021	cttctccaattt 1032	
RESULT 11			
AAZ47894			
ID	AAZ47894 standard; cDNA; 939 BP.		
XX	AAZ47894;		
XX	10-MAR-2000 (first entry)		
XX			

DE	Human protein encoding cDNA SEQ ID NO:5.
XX	
KW	Human; haematopoietic cell regulation; tissue generation; reparation;
KM	activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW	receptor; ligand; autoimmune; infection-related immunodeficiency;
KW	inflammatory disorder; neurological disease; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..939
FT	/tag= a
XX	/note= "no stop codon given"
PN	WO9958668-A1.
XX	
PD	18-NOV-1999.
XX	
PX	13-MAY-1999; 99WO-JP02485.
XX	
PR	14-MAY-1998; 98JP-0131815.
XX	
PA	(ONCY) ONO PHARM CO LTD.
XX	
PI	Fukushima D, Shibayama S, Tada H;
XX	
DR	WPI; 2000-062298/05.
DR	P-PSDB; AAY57602.
XX	
PT	New polypeptides of human origin having cell regulatory, tissue
PT	generation, coagulant and other activities -
XX	
PS	Claim 4; Page 48; 84pp; Japanese.
XX	
CC	The present sequence encodes a specifically claimed novel human protein.
CC	The novel human protein can be used in therapeutic drugs for the
CC	Prevention and treatment of a broad range of disorders including
CC	autoimmune and infection-related immunodeficiency, inflammatory
CC	disorders, and neurological diseases. The novel protein is expected of
CC	having haematopoietic cell regulatory activity, tissue generation/ reparation activity, activin/inhibin activity, taxis/chemotaxis activity, blood coagulation and thrombus activity, and receptor/ligand activity.
CC	
CC	
XX	
SQ	Sequence 939 BP; 245 A; 255 C; 249 G; 190 T; 0 other:
Query Match	55.5%; Score 939; DB 21; Length 939;
Best Local Similarity	100.0%; Pred. No. 1.4e-226;
Matches 939; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	223 cgcagcggagatgccacctccccaaagtctgacaaactgtacggtccggcaggggag 282 Db 1 cgcagcggaagtgtccacctccccaaagtctgacaaactgtacggtccggcaggggag 60
QY	283 agcgccaccctcagtgtaatttgaacaaccggtcaaccgggtgacctgtgtctaacccg 342 Db 61 agcgccaccctcagtgtaatttgaacaaccggtcaaccgggtgacctgtgtctaacccg 120
QY	343 agcacctcctctatgtctgggaatgatcaaatgtgtgacctgtatcttcgctctctg 402 Db 121 agcacctcctctatgtctgggaatgatcaaatgtgtgacctgtatcttcgctctctg 180
QY	403 agcaaccaccaaacgcagttacagcatgagatccagaactgtgatatgacgagggc 462 Db 181 agcaaccaccaaacgcagttacagcatgagatccagaactgtgatatgacgagggc 240
QY	463 ccttacacctgtcgtgtgacagacagacaaccaccaagaactctagggtccaactcaat 522 Db 241 ccttacacctgtcgtgtgacagacagacaaccaccaagaactctagggtccaactcaat 300
QY	523 gtgcaagatctcccacaattgtagagattcttcagatatctccaatgaagggaac 582 301 gtgcaagatctcccacaattgtagagattcttcagatatctccaatgaagggaac 360

QY	583	aataatagcctcaacctgcatagaacaactgtgtagaccagacctaacgttactcttggaagaac	642
Dd	361	aataatagcctcaacctgcatagaacaactgtgtagaccagacctaacgttactcttggaagaac	420
QY	643	atctctcccaaagcggttggtcttgtgagtgaagacgaatacttggaaattcagggcac	702
Dd	421	atctctcccaaagcggttggtcttgtgagtgaagacgaatacttggaaattcagggcac	480
QY	703	accccggaagcagtcaggggactacgagtgcagttgcctccaatgacgttgccgcgccgtg	762
Dd	481	accccggaagcagtcaggggactacgagtgcagttgcctccaatgacgttgccgcgccgtg	540
QY	763	gtacggagagtaaaagtlcacccgtgaactatccaccaatattcagaagccaaggtaca	822
Dd	541	gtacggagagtaaaagtlcacccgtgaactatccaccaatattcagaagccaaggtaca	600
QY	823	ggtgtccccgtgggacaaaaaggggacactgcacgtgtgaagcctcagcagfcccctcagca	882
Dd	601	ggtgtccccgtgggacaaaaaggggacactgcacgtgtgaagcctcagcagfcccctcagca	660
QY	883	gaattccagtggttcacaaggatgcacaaaaagactgattgaagagaaagaaggggtgaagaatg	942
Dd	661	gaattccagtggttcacaaggatgcacaaaaagactgattgaagagaaagaaggggtgaagaatg	720
QY	943	gaaaacagaccttctcctctcaaaaactatcttcttcaatgtctctgaaacatgatggg	1002
Dd	721	gaaaacagaccttctcctctcaaaaactatcttcttcaatgtctctgaaacatgatggg	780
QY	1003	aactaacttgcgtyggcgctcccaacaagctggggccacaccaaatgccaagcatatgtattt	1062
Dd	781	aactaacttgcgtyggcgctcccaacaagctggggccacaccaaatgccaagcatatgtattt	840
QY	1063	ggtccagggcgccgttcagcgaggtgtagcaacgggcacgctcgagagagggcagggctgcttg	1122
Dd	841	ggtccagggcgccgttcagcgaggtgtagcaacgggcacgctcgagagagggcagggctgcttg	900
QY	1123	ctgctgcctctctctggtcttgacactgcttctcaaat	1161
Dd	901	ctgctgcctctctctggtcttgacactgcttctcaaat	939

XX	RESULT 12
AAAA44536	
ID	AAAA44536 standard; cDNA; 832 BP.
XX	
AC	AAAA44536;
XX	
DT	21-AUG-2000 (first entry)
XX	
DE	Human secreted expressed sequence tag SEQ ID NO:1111.
XX	
KW	Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
KW	expressed sequence tag; EST; probe; chemotactic; proliferative;
KW	immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW	thrombolytic; antiinflammatory; cytosolic; antibacterial; antifungal;
KW	antiviral; antidiabetic; antiasthmatic; vulnerrary; antiparkinsonian;
KW	antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW	cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW	vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW	insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW	lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW	central nervous system disorder; Alzheimer's disease; stroke;
KW	Parkinson's disease; Huntington's disease; coagulation disorder;
KW	haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW	tumour; infection; depression; psoriasis; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200021991-A1.
XX	
PD	20-APR-2000.
XX	

PF 15-OCT-1999; 99WO-US24206.
XX
PR 15-OCT-1998; 98US-0104436.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-317938/27.
XX
PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (ESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
XX
PS Claim 1; Page 487-488; 803pp; English.

AA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytosstatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerrary; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.

```

Sequence 832 BP; 246 A; 217 C; 206 G; 163 T; 0 other;
SQ
Query Match          46.5%; Score 787.8; DB 21; Length 832;
Best Local Similarity 99.6%; Pred. No. 1.7e-18;
Matches 800; Conservative 0; Mismatches 2; Indels 1; Gaps 1
QY 1 gtccctcagcaaaaacagtgatlttaatctctcttgcaacaagcttgagagcaacaatct 60
    |||||
Db 27 gtccctcagcaaaaacagtgatlttaatctctcttgcaacaagcttgagagcaacaatct 86
QY 61 atcaggaagaagaagaagaagaagaacccgaacctgacacaaaaagaagaagaagaaga 120
    |||||
Db 87 atcaggaagaagaagaagaagaagaacccgaacctgacacaaaaagaagaagaagaaga 145
QY 121 aaaaaaatcatgaaaaaaccatccagccaaaaaatgacaaattctatctcttgygcaatcttc 180
    |||||
Db 146 aaaaaaatcatgaaaaaaccatccagccaaaaaatgacaaattctatctcttgygcaatcttc 205
QY 181 acggggtgctgctgtctgtgtctcttccaaggagtgccggctgcgcaaggagatgccacc 240
    |||||
Db 206 acggggtgctgctgtctgtgtctcttccaaggagtgccggctgcgcaaggagatgccacc 265
QY 241 ttccccaagaagctatygacaacagtgacggtcccggcaggggagagcgccaccctcaggtgc 300
    |||||
Db 266 ttccccaagaagctatygacaacagtgacggtcccggcaggggagagcgccaccctcaggtgc 325
QY 301 actattgacaacccggtcacaccgggtgacctggtctaacaaccgcagcaccaatccttatgct 360
    |||||
Db 326 actattgacaacccggtcacaccgggtgacctggtctaacaaccgcagcaccaatccttatgct 385
QY 361 gggaataagcaactgtatccctatgatacttcgcatgattccttctgaagcaaacaccacacgac 420

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|||||
Db 386 gggaatgacaagtgtgctgtgatccctgcgtgtgtcccttcttgagaacacccaacgcag 445
QY 421 tacagcatcgagatccagaacgctggtatgtatgacagggcccttacacctgtcgtg 480
Db 446 tacagcatcgagatccagaacgctggtatgtatgacagggcccttacacctgtcgtg 505
QY 481 cagacagacacacccacaaagacctctgaggtccacctcatgtgtgcaagtatctcccaa 540
Db 506 cagacagacacacccacaaagacacctctgaggtccacctcatgtgtgcaagtatctcccaa 565
QY 541 attgtagagatttcttcagatatctccaatatgaagggaacaatatagcctcactgc 600
Db 566 attgtagagatttcttcagatatctccaatatgaagggaacaatatagcctcactgc 625
QY 601 atagcaactggttagaccagaagcctacggttactcttgagagacacatctctccaaacggtt 660
Db 626 atagcaattgttagaccagaagcctacggttactcttgagagacacatctctccaaacggtt 685
QY 661 ggccttgtgagtgaagacgaataacttgaaattcagggcatcacccgggagcagtcagg 720
Db 686 ggccttgtgagtgaagacgaataacttgaaattcagggcatcacccgggagcagtcagg 745
QY 721 gactacgagtgcagtgccctccaatgacgtgcccgcgcgtgtgtacggagagtaagagtc 780
Db 746 gactacgagtgcagtgccctccaatgacgtgcccgcgcgtgtgtacggagagtaagagtc 805
QY 781 accgtgaactataccaccatacat 803
Db 806 accgtgaactataccaccatacat 828

RESULT 13
AA051015

ID AA051015 standard; cDNA; 3069 BP.

XX AC AA051015;

XX DT 17-MAY-1994 (first entry)

XX DE Rat opioid receptor gene.

XX KW Transgenic; narcotics; analgesics; expression; antisense therapy;
KW analogue; derivative; degradation; chronic pain; cancer; morphine;
XX detection; diagnosis; additicts; ds.

OS Rattus rattus.

XX PN W09321309-A.

PD 28-OCT-1993.

XX PF 29-MAR-1993; 93WO-US02913.

XX PR 10-APR-1992; 92US-0866677.

XX PA (LEEN/) LEE N M.
XX PA (LIPP/) LIPPMAN D.
XX PA (LOHH/) LOH H H.

XX PI Lee NM, Lippman D, Loh HH;

XX DR WPI; 1993-351719/44.

XX PT Transgenic animals and novel oligo-nucleotide constructs - useful
XX in diagnosis and treatment of addiction to narcotic analgesics

XX PS Claim 5; Page 25-30; 49pp; English.

CC The sequence is that of the rat opioid receptor gene. The gene is
CC able to hybridise with endogenous mRNA for an opioid binding protein
CC to suppress expression of an opioid receptor gene. Transgenic
CC animals contg. the gene in reverse are useful in diagnosis and

CC treatment for addiction to narcotic analgesics. By admin. of
CC antisense fragments of the gene, chronic pain, such as in terminal
CC cancer patients can be treated without development of tolerance to
CC analgesics such as morphine. The gene may aslo be used
CC diagnostically to detect addicts.
XX See also AA051016-7.

XX SQ Sequence 3069 BP; 803 A; 787 C; 661 G; 818 T; 0 other;

Query Match 31.9%; Score 540.8; DB 14; Length 3069;
Best Local Similarity 71.2%; Pred. No. 5.4e-126;
Matches 729; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 149 aaatgcacaattctatctcttggcgaatcttcacggggtgctgtctctctcc 208
Db 636 agatgtaccatcccgctactgtagctctctctggccaccacgacctgtcttcaccc 695
QY 209 aaggagtcccgctgcgcagcggagatgccaccttccccaagctatggacaagtgcag 268
Db 696 caggagtcccgctgcgcagcggagatgccaccttccccaagctatggacaagtgcag 755
QY 269 tccgcagggggagagcgccaccctcagtgtaactattgacaacgggtcacccgggtg 328
Db 756 tccgcagggggagagcgccaccctcagtgtaactattgacaacgggtcacccgggtg 815
QY 329 cctggctaaccgcgacgaacccatccctatgctggtgaatgacaagtgtgcctgatac 388
Db 816 cctggctaaccgcgacgaacccatccctatgctggtgaatgacaagtgtgcctgatac 875
QY 389 gcgtgtcctcttgagcaacaccccaacgcagtaagcatcgagatccagaacgtgatg 448
Db 876 gagtgtatcatcttgtaacacgcgtaccagtaagcatcgagatccagaacgtgatg 935
QY 449 tgtatgacgagggcccttaacacctgtcgtgtgcagacagacacccaagacctcta 508
Db 936 ttatgacgagggcccttaacacctgtcgtgtgcagacagacacccaagacctccc 995
QY 509 ggtgccacctcatgtgtgaagtatctcccaaatgttagagatttctcagatatctcca 568
Db 996 ggtgccacctcatgtgtgaagtatctcccaagataatgaacatctctcagacattact 1055
QY 569 ttaatgaagggaacaatttagcctcactgcataagcaactgtgtaaccagagcctac 628
Db 1056 tgaatgagataagcagtgtagccttgttattgtctgcgaattggcagaccagaacca 1115
QY 629 ttacttgagaacacatctctccca--aagcggttgcttgtgtgaagtgaagcaatact 685
Db 1116 tgacatgycgacacctgtcagtaaggaagccaagcgcttgtgtgaagtgaataacc 1175
QY 686 tgyaaattcagggcatcacccgggagcgactcaggggaactacgagtgcagtcctcca 745
Db 1176 tgyaaattcagggcatcacccgggagcgactcaggggaactacgagtgcagtcctcca 1235
QY 746 acgtgcccgcgcgtgtgtacgagagtaaaagtcaaccgtgaactataccaccatactt 805
Db 1236 atgtcgtcgcacctgatgttcggaagtaaaatacactgttaacctatccctatatct 1295
QY 806 cagaagccaaggttacaggtgtcccgctgggacaagaagggacactgtcagtgtaagcct 865
Db 1296 caaagcgagaagaacactgycgttccagtaggccagaagggcatcctgagctgtga 1355
QY 866 cagcagtcctccctcagcagaattccagtgtgtaagaagtgaacaagactgatgaagg 925
Db 1356 ctgtgtcccatggtgtgaattccacgtgtgttaaggaagataccaggttagccaactg 1415
QY 926 agaaaggggtgaagtgtgaacaagaccccttcctcacaactcattcttccatgtct 985
Db 1416 tgyatgctgtgagaattgagaacaagggccgcatatccacttgcatttcttcaatgt 1475
QY 986 ctgaacatgactatgtgaactatacactgtgtgcttccacaagaagctgggccacca 1045
Db 1476 cagagaagattatgtggaactatacctgtgtgtgccacaagaagcttgggaacca 1535

DE Rat opioid receptor gene.
XX
KW Transgenic; narcotics; analgesics; expression; antisense therapy;
KW analogue; derivative; degradation; chronic pain; cancer; morphine;
KW detection; diagnosis; addicts; ds.
XX
OS Rattus rattus.
XX
PN WO9321309-A.
XX
PD 28-OCT-1993.
XX
PF 29-MAR-1993; 93WO-US02913.
XX
PR 10-APR-1992; 92US-0866677.
XX
PA (LEEN/) LEE N M.
PA (LIPP/) LIPPMAN D.
PA (LOHH/) LOH H H.
XX
PI Lee NM, Lippman D, Loh HH;
XX
DR WPI; 1993-351719/44.
XX
PT Transgenic animals and novel oligo-nucleotide constructs - useful
PT in diagnosis and treatment of addiction to narcotic analgesics
XX
PS Claim 5; Page 30-3; 49pp; English.
XX
CC The sequence is that of the rat opioid receptor gene. The gene is
CC able to hybridise with endogenous mRNA for an opioid binding protein
CC to suppress expression of an opioid receptor gene. Transgenic
CC animals contg. the gene in reverse are useful in diagnosis and
CC treatment for addiction to narcotic analgesics. By admin. of
CC antisense fragments of the gene, chronic pain, such as in terminal
CC cancer patients can be treated without development of tolerance to
CC analgesics such as morphine. The gene may also be used
CC diagnostically to detect addicts.
CC See also AA051015-7.
XX
SQ Sequence 2337 BP; 581 A; 578 C; 520 G; 658 T; 0 other;

Query Match 30.9%; Score 523; DB 14; Length 2337;
Best Local Similarity 72.2%; Pred. No. 1.4e-121;
Matches 695; Conservative 0; Mismatches 265; Indels 3; Gaps 1;
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Db 547 aggaagtgcccgtagcgagagatgcccacctccccaagctatgacaacgtgacggt 606
QY 270 ccggcagggggagagcgccacctcagtgactattgcaaccgggtcacccgggtggc 329
Db 607 ccggcagggggagagcgccacctcagtgactattgcaaccgggtcacccaggatgc 666
QY 330 ctggctaaaccgagcaccatctctatgtggygaatgacaagtgtgctgtgacccctcg 389
Db 667 ctggctaaaccgagcaccatctctatgtggygaatgacaagtgtgctcatagaccctcg 726
QY 390 cgtggtcctctgagcaaacaccacaagcagtagcagcatcgatccagaacgtgagtgt 449
Db 727 agtgatcatcttgtagcaaacagcctacccagtagcatgatatgacagaaatgtgagt 786
QY 450 gtatgacgagggccttacacctgtcgtgtagacagacaaccaccaagacaccttag 509
Db 787 ttaagacgaaggtccgtacacctgtctgtgtagacagacaatcaccccaaacctcccg 846
QY 510 ggtcacacctatgtgcaagtatctcccaaatgttagagatttctcagatatctcat 569
Db 847 ggtcacacctatgtgcaagtatctcccaagataatgaacatctctcagacattactgt 906
QY 570 taatgaagggaacaatatagacctcactgcatagcaactggttagaccagagacctaggt 629

Db 907 gaatgagataagcagtgtagaccttgtagtctgcgaattgycagaccagaaccaacaggt 966
QY 630 tacttggagacacatctctccca---aagcggttggttgtagtgaagacgaactt 686
Db 967 gacatggcgacacacctgtcagtaaggaaggccagggtctgtgtaggaagtgaactac 1026
QY 687 ggaattcagggtcatccaccggagcagtagtcagggtactaagtagtgcctccaatga 746
Db 1027 ggaatctcagacatcaaacgcgaccacatctgagagtagtagtgcagcgacctgaatga 1086
QY 747 cgtggcggcccgtagtagcaggaagtaaggtcacccgtgaactatccaccataattc 806
Db 1087 tgtcgtgacacctgtagtgcgnaagtaaaaatcacgtgtaactatccctccatatactc 1146
QY 807 agaagccaagggtagcaggtgtcccgtaggacaagaaggagacactgagtgtaggcctc 866
Db 1147 aaaagcgaagaaacactgtagtctcagtagccaggaaggacatccctgagctgtaggcctc 1206
QY 867 agcagtcacctcagcagaattccagtggtacaaagtagacaagaagactgattgaagaaa 926
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QY 927 gaaaggggtgaaagtggaaaaacagaccttctctcaaaactcatcttctcaatgtctc 986
Db 1267 gtagtgcgtgtagaattgagaacaaggccgcgcatatccactttagacttctcaagtctc 1326
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Db 1327 agagaagtagtattggaactatacctgtgtgccaacaacaagcttgggaaccaaatgc 1386
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QY 1167 tga 1169
Db 1507 aga 1509

Search completed: July 11, 2002, 23:01:30
Job time: 8958 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 18:35:21 ; Search time 2986.73 Seconds
(without alignments)
4663.581 Million cell updates/sec

Title: US-09-700-397-1
Perfect score: 1032
Sequence: 1 atgaataaccatccagcccaaa.....tgcacctgtcttcaattt 1032

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	635.2	61.6	1039	10	BE798585	BE798585 601581610
2	541	52.4	865	10	BI666583	BI666583 603291469
3	531.4	51.5	545	10	BE263639	BE263639 601192064
4	521	50.5	732	10	BI551784	BI551784 603197479
5	507	49.1	1015	9	AL533026	AL533026 AL533026
6	495.4	48.0	784	10	BI549918	BI549918 603194765
7	494.8	47.9	580	10	BI548566	BI548566 603189502
8	463	44.9	768	9	AU080629	AU080629 AU080629
9	462	44.8	661	10	BM009450	BM009450 603629962
10	462	44.8	953	10	BM423716	BM423716 AGENCOURT
11	457.4	44.3	524	9	BE014142	BE014142 125737 MA
12	455	44.1	979	10	BG261691	BG261691 602373361
13	450	43.6	849	10	BI755360	BI755360 603024964
14	447.6	43.4	553	10	BE864555	BE864555 UI-M-BH1-
15	423.2	41.0	633	10	BG706987	BG706987 602672194
16	411.4	39.9	754	10	BI598759	BI598759 603245538
17	408.8	39.6	671	9	BB644996	BB644996 BB644996

18	404.2	39.2	557	10	BM256660	BM256660 520043 MA
19	396.8	38.4	533	10 <th>BI341675</th> <th>BI341675 369186 MA</th>	BI341675	BI341675 369186 MA
20	388.8	37.7	754	10 <th>BI550038</th> <th>BI550038 603192502</th>	BI550038	BI550038 603192502
21	371	35.9	705	10 <th>BG704152</th> <th>BG704152 602687364</th>	BG704152	BG704152 602687364
22	356.8	34.6	683	9 <th>BB640070</th> <th>BB640070 BB640070</th>	BB640070	BB640070 BB640070
23	347.2	33.6	548	9 <th>BE015245</th> <th>BE015245 127482 MA</th>	BE015245	BE015245 127482 MA
24	344	33.3	806	9 <th>AU051132</th> <th>AU051132 AU051132</th>	AU051132	AU051132 AU051132
25	336	32.6	522	10 <th>BI553032</th> <th>BI553032 603193672</th>	BI553032	BI553032 603193672
26	328.8	31.9	688	9 <th>BB646531</th> <th>BB646531 BB646531</th>	BB646531	BB646531 BB646531
27	325	31.5	329	10 <th>F06205</th> <th>F06205 HSC10F041 n</th>	F06205	F06205 HSC10F041 n
28	323.4	31.3	655	10 <th>BI548049</th> <th>BI548049 603196558</th>	BI548049	BI548049 603196558
29	310.2	30.1	602	9 <th>BB611718</th> <th>BB611718 BB611718</th>	BB611718	BB611718 BB611718
30	295	28.6	764	10 <th>BI752729</th> <th>BI752729 603028343</th>	BI752729	BI752729 603028343
31	291.6	28.3	415	10 <th>R18841</th> <th>R18841 Y922906.r1</th>	R18841	R18841 Y922906.r1
32	290	28.1	290	10 <th>F05894</th> <th>F05894 HSC0PH101 n</th>	F05894	F05894 HSC0PH101 n
33	288.8	28.0	567	10 <th>BE078551</th> <th>BE078551 228917 MA</th>	BE078551	BE078551 228917 MA
34	286.2	27.7	497	9 <th>BB854833</th> <th>BB854833 BB854833</th>	BB854833	BB854833 BB854833
35	285.6	27.7	579	9 <th>BB644523</th> <th>BB644523 BB644523</th>	BB644523	BB644523 BB644523
36	284.2	27.5	528	9 <th>BB856778</th> <th>BB856778 BB856778</th>	BB856778	BB856778 BB856778
37	261	25.3	456	9 <th>AI369684</th> <th>AI369684 qy71903.x</th>	AI369684	AI369684 qy71903.x
38	238	23.1	282	10 <th>R75391</th> <th>R75391 MDB0556R MO</th>	R75391	R75391 MDB0556R MO
39	235.6	22.8	788	10 <th>BI767217</th> <th>BI767217 603057906</th>	BI767217	BI767217 603057906
40	235.4	22.8	492	9 <th>AW967001</th> <th>AW967001 EST379075</th>	AW967001	AW967001 EST379075
41	231.8	22.5	277	10 <th>BI011319</th> <th>BI011319 QV2-EN009</th>	BI011319	BI011319 QV2-EN009
42	220	21.3	444	9 <th>AA682970</th> <th>AA682970 ae89a04.s</th>	AA682970	AA682970 ae89a04.s
43	210	20.3	229	9 <th>AA450172</th> <th>AA450172 zx42d09.r</th>	AA450172	AA450172 zx42d09.r
44	209	20.3	257	9 <th>AW327110</th> <th>AW327110 20640 MAR</th>	AW327110	AW327110 20640 MAR
45	208.4	20.2	1148	10 <th>BM466102</th> <th>BM466102 AGENCOURT</th>	BM466102	BM466102 AGENCOURT

ALIGNMENTS

RESULT 1
BE798585
LOCUS BE798585 1039 bp mRNA linear EST 20-SEP-2000
DEFINITION 601581610F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3935955 5',
mRNA sequence.
ACCESSION BE798585
VERSION BE798585.1 GI:10219783
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1039)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM779 row: d column: 04
High quality sequence stop: 849.
FEATURES
source
1. 1039
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3935955"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

BASE COUNT	ORIGIN
274 a	the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
271 c	286 g
207 t	1 others

Query Match	61.6%;	Score 635.2;	DB 10;	Length 1039;
Best Local Similarity	97.6%;	Pred. No. 5.9e-161;		
Matches 656; Conservative	0;	Mismatches 13;	Indels 3;	Gaps 1;

QY	165	caagtgacatctatcgacaacaccgggtcaccggggtggtcctgtgctctaaaccgcagcaccatcct	224
Db	65	CAGGTGCACCTATTGACAAACCGGGGTGCCCGGGGTGGCTTAAACCGCAGCACCATTCCT	124
QY	225	ctatgctygaatgacaagltggtgctgtgatcctgcgtgtgtctctctagcaacaacca	284
Db	125	CTATGCTGGGAATGACAAAGTGGTGCTGGATCCTGCGGTGCTCTGTGAGCAACACCCA	184
QY	285	aacgcagtacagatcagatccagaacgltgtaigtltatgaagaggccctacacctg	344
Db	185	AACGCAGTACAGCATCGAGATCCAGAACTGGATGTGTATGACGAGGGCCCTTACACCTG	244
QY	345	ctcgtgtagacagacaaccaccaagaacctctaggggtccacctcatgtgtgcaagtac	404
Db	245	CTCGGTGCAGACAGACAACCAACCAAGACCTCTAGGGTCCACCCCATTTGTGCAGTATC	304
QY	405	tcccaaatgttagagatttcttcaatatctccattaatgaaggaacaatatatgacct	464
Db	305	TCCCAAAATGTAGAGATTCTTCCAGATATCTCCATTATGAAGGAACAATATTAGCCT	364
QY	465	caactgcataagcaactgtgtagaccagagcctaaggttacttggagacacatctctccaa	524
Db	365	CACCTGCATAGCAACTGGTAGACCAAGCCTAACGTTACTTGGAGACACATCTTCCCAA	424
QY	525	agcgtgtgcttgtgtagtgaagacgaatacttggnaattcaaggcatcaaccggagaca	584
Db	425	AGCGGTTGGCTTGTGAGTGAAGACGAATACCTTGAATTTCAGGGCATCCACCCGGAGCA	484
QY	585	gtcaggggactacagtgtagtgcgtgcctccaatgacgtgcccgcgccgtgtgtacggaagt	644
Db	485	GTCAGGGGACTACAGTGCAGTGCCTCCCAATGACGTGGCCGCCCGCTGTACGGAGAGT	544
QY	645	aaagtcacgctgnaactatccaccatacttccagaagccaaggytaccaggtgtccccgt	704
Db	545	AAAGGTCACCGTGAACATATCCACCATACTTTCAGAAAGCCCAAGGGTACAGGTGTCCCGCT	604
QY	705	gggacaaaaggggacacactgcagtgtgaaagcctcagccagtcgccctcagcagaattccagt	764
Db	605	GGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAATTCCAGTG	664
QY	765	gtacaagatgtacaaaagactgtatgaaagaa--agaaaggygtgtaaagtgtgaaaacag	821
Db	665	GTACAGGATGACAAAGACTGATGTGAAGGACACAGCAGGGGTGAACAGTTGGAAACACAG	724
QY	822	acccttcctctc 833	
Db	725	ACCTTTTTCCTC 736	
RESULT	2		
BI666583			
LOCUS		865 bp	mRNA
DEFINITION	603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',		linear
	mRNA sequence.		EST 12-SEP-2001
ACCESSION	BI666583		
VERSION	BI666583.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 865)		

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM11787 row: j column: 18
 High quality sequence stop: 742

FEATURES	Location/Qualifiers
source	1. .865

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5310833"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTCTT-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

```

Query Match	52.4%	Score 541	DB 10	Length 865
Best Local Similarity	99.8%	Pred. No. 1.7e-135		
Matches 552	Conservative 0	Mismatches 0	Indels 1	Gaps 1
QY 1	atgaaaaccatccagccaaaatgcaaatctatctcttgygcaatcttcagggctg	60		
Db 183	ATGAAAACCATCCAGCCAAAATGCACAATTCTATCTTGGCAATCTTCACGGGGCTG	242		
QY 61	gctgctctgtgtctcttccaaagatgcccgtgcccagcggagatgcccacttcccaaa	120		
Db 243	GCTGCTCTGTGTCTCTTCCAAAGAGATGCCCGGTGCCGACGGGAGATGCCACCTTCCCAAA	302		
QY 121	gctatgacaacagtgaaggtccgycagggggagagcgcaccctcagtgcaatttgac	180		
Db 303	GCTATGGACACAGTGACGGTCCGGCAGGGGGAGAGCGCCACCCCTCAGGTGCACATTTGAC	362		
QY 181	aaccgggtcaccggggtgctgctgctaaccgcagcaccatctcttctgtggaatgac	240		
Db 363	AACCGGGTCACCGGGTGGCTGGCTTAAACCGACACCATCTCTATGCTGGGAATGAC	422		
QY 241	aagtgtgacctgcatcctgcgcgtgtgtctctctgagcaacaaccaacgcagtagcagc	300		
Db 423	AAGTGTGCTTGATCCTCGCGTGGTGTCTTGAGCAACACCCAAACGAGTACAGCATC	482		
QY 301	gagatccagaacgttgatgtgtatgacagaggcccttaccactgtctcgtgacagacag	360		
Db 483	GAGATCCAGAACGTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	542		
QY 361	aaccacccaaaagacctctaggtgccactcatltytgcaagtatctcccaaaattgtagag	420		
Db 543	AACCAACCCAAAGACCTCTAAGGGTCCACCTCATTTGTCAAGTATCTCCAAAATTGTAGAG	602		
QY 421	attctctcagatatctccattaatgaagggaac-aatatlagcctcactgcataagcaac	479		
Db 603	ATTCTTCAGATATCTCCATTAAATGAAGGGAACAATAATTAGCCCTCAGCTGCATAGCAAC	662		
QY 480	tggttagaccagagccttaagcttacttggagacacatctctcccaaaagcgttggctttgt	539		

|||||
 Db 663 TTGTTAGACCAAGCCTACGTTACTTGTGAGACACATCTCTCCCAAGCGGTGGCTTTGT 722
 QY 540 gaagtaagacgaa 552
 |||||
 Db 723 GAGTGAAGACGAA 735

RESULT 3
 BE263639 545 bp mRNA linear EST 13-JUL-2000
 LOCUS 601192064F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3536127 5',
 DEFINITION mRNA sequence.
 ACCESSION BE263639
 VERSION BE263639.1 GI:9137183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 545)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Plate: L16M217 row: p column: 16
 High quality sequence stop: 545.

FEATURES
 source
 1..545
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3536127"
 /clone_1id="NIH_MGC_7"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 162 a 134 c 144 g 105 t
 ORIGIN

Query Match 51.5%; Score 531.4; DB 10; Length 545;
 Best Local Similarity 99.6%; Pred. No. 5.3e-133;
 Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 271 ctgagcaaccacccaacgcaagctacacatcgaagcgaagcgtggtatgtatgacgag 330
 |||||
 Db 1 CTGAGCAACACCCCAAGCGAGTACAGCATCGAGATCCAGACGTGATGTATGACGAG 60
 QY 331 ggccttacaacctgtcgtggtgagacagacaacacccaagaacctctaggtcacctc 390
 |||||
 Db 61 GGCCCTTACACCTGCTGGGTGCAGACAGACAACCAAGACCTCTAGGGTCCACCTC 120
 QY 391 attgtgcaagtatctcccaaaattgttagagattcttcagatatctccattatgaagg 450
 |||||
 Db 121 ATTGTGCAAGTATCTCCCAAAATGTAGAGATTCTTCAGATATCTCCATTATGAAGG 180
 QY 451 aacaatatagcctcacctgcataagcaactgtagaccagagcctacggttacttgaga 510
 |||||
 Db 181 AACAAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAAGAGCCTTACGTTACTTGAGA 240
 QY 511 cacatcttcccaaaagcggttgcttgtgagtgaagaagcaatacttggaaattcagggc 570
 |||||
 Db 241 CACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 300

QY 571 atcacccggagcagtcacggagcactacagtgacgtgcctccaatgacgtgcccgc 630
 |||||
 Db 301 ATCACCAAGGAGCAGTACGAGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGCGCGGCC 360
 QY 631 gtgtacgagagtaaggtcacccgtgaactatccaccatattcagaagccaaggt 690
 |||||
 Db 361 GTGTACCGAGAGTAAAGCTCACCGGTGAACACTATCCACCATATTCAGAAAGCAAGGT 420
 QY 691 acaggtgtcccgctggagcaaaaaggagacactgcagtggtgaagcctcagcgtccctca 750
 |||||
 Db 421 ACAGGTGTCCCGCTGGGACAAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCA 480
 QY 751 gcagaattccagtggtacaaagatgacacaaagactgattgaaggaa-gaaaggggtgaa 809
 |||||
 Db 481 GCAGAATTCAGTGTGTACAAAGATGACAAAGACTGATTGAAGGAACGAAGCGGTGAA 540
 QY 810 agtgg 814
 |||||
 Db 541 AGTGG 545

RESULT 4
 B1551784 732 bp mRNA linear EST 05-SEP-2001
 LOCUS B1551784
 DEFINITION 60319747F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5277115 5',
 mRNA sequence.
 ACCESSION B1551784
 VERSION B1551784.1 GI:15439096
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 732)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L16M1699 row: m column: 20
 High quality sequence stop: 732.

FEATURES
 source
 1..732
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5277115"
 /clone_1id="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTTT-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 218 a 191 c 172 g 150 t 1 others
 ORIGIN

Query Match 50.5%; Score 521; DB 10; Length 732;
 Best Local Similarity 99.5%; Pred. No. 4.1e-130;
 Matches 543; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 atgaaacacatccagccaaatgacaaatctctcttgggcaatcttcacgggctg 60
 Db 188 ATGAAAACCATCCAGCCAAAATGACAAATTCATCTCTTGGCAATCTTCACGGGCTG 247
 QY 61 gctgctgtgtctcttccaagagtgccctgacgagcgagatgccacttcccaaa 120
 Db 248 GCTGCTGTGTCTCTTCCAAGAGAGGCCGCTGGCAGCGAGATGCCACCTTCCCAAAA 307
 QY 121 gctatgacacatgacggtgcccggagggagagcgccaccctcagtgacatttgac 180
 Db 308 GCTATGACACATGACGGGTCCCGGAGGGGAGAGCGCCACCTCAGGTGCACTATGAC 367
 QY 181 aaccgggtacccgggtggtgctgctaaacccgacacacatctctatgtggaatgac 240
 Db 368 AACCGGTCACCCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 427
 QY 241 aagtgtgctgtgacccctgctgctctcttgagcaacaccccaaacgagtcacgacac 300
 Db 428 AAGTGTGCTGTGATCTCGCGTGGCTCTTCTGAGCAACACCCAAACGACATCAGCATC 487
 QY 301 gagatccagaacgtgagtgatgacagagggcccttaacactgtctggtgcagacagac 360
 Db 488 GAGATCCAGAACGTGAGTGTATGACAGAGGGCCCTTACACCTGCTGGTGACAGACAG 547
 QY 361 aaccacccaaagacctagaggtccacactcatgtgcaagtatccccaaatgtagag 420
 Db 548 AANCAACCAAGACCTTAAGGGTCCACCTCATGTGCAAGTATCTCCAAAATGTAGAG 607
 QY 421 attcttcagatatctcctaataatgaagggaacaatatagcttcacactgcatagaact 480
 Db 608 ATTCTTCAGATATCTCATTAATGAAGGGAACAATATAGCCTCACCTGCATAGCAACT 667
 QY 481 ggtagaccagagcctacggttacttg-agaacacatctctcccaagcggttgcttgt 539
 Db 668 GTAGACCAAGCCTACGCTTACTTGAAGACACATCTCTCCCAAGCGG-TGGCTTTGT 726
 QY 540 gaagtga 545
 Db 727 GAGTGA 732

RESULT 5
 AL533026 1015 bp mRNA linear EST 13-FEB-2001
 LOCUS AL533026 LTI_FL015_Brn1 Homo sapiens cDNA clone GS0DN005YD20 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL533026
 VERSION AL533026.1 GI:12796519
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1015)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source
 1..1015
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GS0DN005YD20"
 /clone_lib="LTI_FL015_Brn1"
 /sex="male"
 /tissue_type="Adult brain"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was constructed by Life Technologies.
 Contact : Feng Liang Life Technologies, a division of
 Invitrogen 9800 Medical Center Drive Rockville, Maryland
 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 295 a 249 c 251 g 219 t 1 others
 ORIGIN
 Query Match 49.1%; Score 507; DB 9; Length 1015;
 Best Local Similarity 84.3%; Pred. No. 3e-126;
 Matches 635; Conservative 0; Mismatches 0; Indels 118; Gaps 1;

QY 398 aagatctcccaaaattgtagagatttctcagatatctccatgaaggaacata 457
 Db 90 AAGTATCTCCAAAATGTAGAGATTCTTCAATATCTCCATTAATGAAGGAACATA 149
 QY 458 ttagcctcactgcatagcaactgttagaccagcctaaggttacttgagacacatc 517
 Db 150 TTAGCCTCACCTGCATAGCAACTGTAGACCAAGCCTTACGTTACTTGGAGACACATCT 209
 QY 518 ctcccaagcggttgcttgtagtgaagacgaatcttggaatcgaagcatcacc 577
 Db 210 CTCCCAAGCGGTGTGCTTGTGATGAAGACGAATACTTGAATTCAGGCGATCACCC 269
 QY 578 gggagcagtcagggactacgagtgacgtgctcccatgacgtgcccgtgtgtac 637
 Db 270 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCAATGACGTGGCCGCGGTGTGAC 329
 QY 638 gggagtaaaagtgtaacgttgactatccaccatatttcagaagccaaggtacagt 697
 Db 330 GGAGAGTAAGGTTCACCGTGAACATTCACCATATTCAGAAAGCCAAAGGATACAGTG 389
 QY 698 tccccgtgggacaaaaggggacactgagtgtagcctcagcaggtccctcagcagaat 757
 Db 390 TCCCGGTGGACAAAAGGGGACACTGAGTGTGAAGCCTCAGCATCCCTCAGCAGAAT 449
 QY 758 tccagtgtaacaagatgacaaa----- 781
 Db 450 TCCAGTGTACAAAGATGACAAAAGCCTGAATCTCATTCACAGTTTGGTTATGATGG 509
 QY 782 ----- 781
 Db 510 AAAGCTTCCTCCCATAGGTGAGCAATGTTGTAACAAAGGCCAGTGGAATCAGCCT 569
 QY 782 -----gactgattgaaggaagaaaggggtgaagtgaagaaac 819
 Db 570 GACTTGCTGCGAGAATCTCCCGACTGATTTGAAGGAAGAAAGGGGTGAAAAGAAC 629
 QY 820 agaccttcctctcaaaactcatctctcctaattgtctcgaacatgactatggaactac 879
 Db 630 AGACCTTTCCTCTCAAACTCATCTCTTCAATGTCTTGAACATGACTATGGAACTAC 689
 QY 880 acttgctggtcctccaaacagctgggccaacacacacatgccaagcatatgtctatgttcca 939
 Db 690 ACTTGCTGGCTCTCCACAAAGCTGGGCCACACCAATGCCAGCATGTCTATTGGTCCA 749
 QY 940 gggcgctgaagcagagtgtagcaacggcagcgtcgaggaaggcagcgtgctgtgctg 999
 Db 750 GGGCGCTGAGCGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGGCTGCGTCTGCTG 809
 QY 1000 cctctctgtgtcttgacactgcttcaaat 1032
 Db 810 CCTCTGTGTCTTGCACCTGCTTCAAAATT 842

RESULT 6
 B1549918 784 bp mRNA linear EST 05-SEP-2001
 LOCUS B1549918
 DEFINITION 603194765F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274161 5',
 mRNA sequence.

ACCESSION B1549918
VERSION B1549918.1 GI:15437230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 784)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1692 row: b column: 18
High quality sequence stop: 726.

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5274161"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 234 a 211 c 184 g 155 t
ORIGIN

Query Match 48.0%; Score 495.4; DB 10; Length 784;
Best Local Similarity 98.0%; Pred. No. 3.6e+123;
Matches 534; Conservative 0; Mismatches 6; Indels 5; Gaps 3;

QY 1 atgaanaccatccagccaaaatgcacaattctatctcttgagcaatcttcacgggctg 60
|||||
DB 193 ATGAANACCATCCAGCCAAATGCACAATTCTATCTTGGCAATCTTCACGGGCTG 252
QY 61 gctgctctgtctcttccaaagagtgcccgctgcgcagcgagatgcaaccttcccaaa 120
|||||
DB 253 GCTGCTCTGTCTCTTCCAAAGAGTGCCTGCGCGAGATGCCACCTTCCCAAA 312
QY 121 gctatgacaacgtgacggtccgcaggggagagcgccaccctcagtgacattgac 180
|||||
DB 313 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCCGCCACCTCAGGTGCATATTGAC 372
QY 181 aaccgggtaccccggtgctgctgctaaccgcagcaccatctctatgtggaatgac 240
|||||
DB 373 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 432
QY 241 aagtggtcctgagatcctgcgctggtctctctgagcaacacccaaacgagtagcagc 300
|||||
DB 433 AAGTGGTCCGTGATCCCTGCGCTGTCTCTTGAGCAACACCAACGAGCAGTACAGCATC 492
QY 301 gagatccagaacgtgagatgtagagagggcccttaacacctgctggtgacagagac 360
|||||
DB 493 GAGATCCAGAACGTGATGCTATGACGAGGGGCCCTTACACCTGCTGGGTGACAGACAG 552
QY 361 aaccacccaagacctaggggtccacctcatgtgcaagtagatctcccaaatgtagag 420

DB 553 AACCAACCCAAAGACCTCTAGGGTCCACCCTCATGTGTGCAAGTATCTCCCAAAA-TGTAGAG 611
|||||
QY 421 attcttcagatatctccattaatgaagggaacaatatattagcctca-ctgcatagcaac 479
|||||
DB 612 ATTCTTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCACCCTGCATAGCAAC 671
QY 480 tggtagacagagcctacggttacttgtagaac--atctctcccaagcggttgctt 536
|||||
DB 672 TGGTAGACAGAGCCTACGGTTACTTGGAGACACCATCTCCCCCAAAAGCGTTGGCTT 731
QY 537 tgtga 541
|||
DB 732 CGCGA 736

RESULT 7
B1548566 580 bp mRNA linear EST 05-SEP-2001
LOCUS 603189502F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5260753 5',
DEFINITION mRNA sequence.
ACCESSION B1548566
VERSION B1548566.1 GI:15435878
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 580)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1657 row: d column: 02
High quality sequence stop: 580.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 172 a 160 c 140 g 108 t
ORIGIN

Query Match 47.9%; Score 494.8; DB 10; Length 580;
Best Local Similarity 99.2%; Pred. No. 4.5e-123;
Matches 518; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 atgaanaccatccagccaaaatgcacaattctatctcttgagcaatcttcacgggctg 60
|||||
DB 60 ATGAANACCATCCAGCCAAATGCACAATTCTATCTTGGCAATCTTCACGGGCTG 119

QY 61 gctgctctgtctcttccaagagtgcccggtgcgcagcgagatgccacctccccaaa 120
 |||||||
 Db 120 GCTGCTCTGTCTCTCTCAAGAGAGTGCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 179
 QY 121 gctatgagc-aacgtgacgttcgcgcaggggagagagccacccctcaggtgacattga 179
 |||||||
 Db 180 GCTATGGACAAACGTGACGCGTCCCGCAGGGGAGAGCGCCACCTCAGGTGACATATGGA 239
 QY 180 caaccggtcaccggtgtgctgtgtaaacccgacgacccatcctctatgtcgggaatga 239
 |||||||
 Db 240 CAACCGGGTCAACCGGGTGGCTTAACCGACGACCATCTCTATGCTGGGAATGA 299
 QY 240 caagtggtgcctggtatcctcgcgtgtgtccttcttgagcaacacccaaacagcagtaacat 299
 |||||||
 Db 300 CAAGTGGTGCCTGGATCCTCGCGTGTCTTCTGAGCAACCCAAACGCACTACAGCAT 359
 QY 300 cgaagatccagaacgtggtatgtatgaagaggcccttaacacctgctcgtgtgcagacaga 359
 |||||||
 Db 360 CGAGATCCAGACGTGATGTGTATGACGAGGGGCCCTTACACCTGCTGGTGACAGACAGA 419
 QY 360 caaccacccaagaacctctaggtgccacctaatgtgcagatattctcccaaatgtaga 419
 |||||||
 Db 420 CAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCCCAAAA-TGTAGA 478
 QY 420 gattcttcagatatctccatlaatgaagggaacaatatagcctcactcgtgcatacgaac 479
 |||||||
 Db 479 GATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCAATAGCAAC 538
 QY 480 tggtagaacagagccttaagcttacttgtagacacatctctcc 521
 |||||||
 Db 539 TGGTAGACCAAGACCTACGGTACTTGAGACACATCTCTCC 580

RESULT 8
 AU080629 768 bp mRNA linear EST 12-JUL-2000
 LOCUS AU080629 Sugano mouse brain mnch Mus musculus cDNA clone MNCb-5883
 DEFINITION 5' mRNA sequence.
 ACCESSION AU080629
 VERSION AU080629.1 GI:6085383
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 768)
 AUTHORS Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A.,
 Suzuki, Y., Sasaki, M. and Sugano, S.
 TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
 library made by oligo-capping method
 JOURNAL Unpublished (1999)
 COMMENT Contact: Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: http://www.nih.go.jp/yoken/genbank/.
 FEATURES
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 1..768
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="MNCb-5883"
 /clone_lib="Sugano mouse brain mnch"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
 was primed with an oligo(dT) primer
 ATGTGGCTTTTCTTTTCTTTT; double-stranded cDNA was
 ligated to a DraIII adaptor (TGTGGCTTACTGG), digested and
 cloned into distinct DraIII sites of the pME18S-FL3. XhoI
 sites just outside the DraIII sites can be used to isolate

the cDNA insert. Size selection was performed to exclude
 fragments <1.5 kb. Library was constructed by Sugano et
 al.(University of Tokyo, Institute of Medical Science).
 Custom primer used for sequencing: 5' end primer
 [CTTCTGCTCTAAAGCTGCG], 3' end primer
 [CGACCTGCAGCTCGAGCACAA]"

BASE COUNT 232 a 190 c 183 g 157 t 6 others
 ORIGIN

Query Match 44.9%; Score 463; DB 9; Length 768;
 Best Local Similarity 91.4%; Pred. No. 2.1e-114;
 Matches 498; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 1 atgaataaccatccagccaaatgacaaattctatctcttggcactcttcagggctg 60
 |||||||
 Db 224 ATGAATAACCATCCAGGCAAAATGCACATCTATCTGTGGCAATCTTCACGGGGCTG 283
 QY 61 gctgctctgtctcttccaagagtgcccggtgcgcagcgagatgccacctccccaaa 120
 |||||||
 Db 284 GCGGCTCTGTGCTCTCTTCCAGGAGTGGCGGTGCGTAGCGGAGATGCCACCTTCCAAA 343
 QY 121 gctatgacaaacgtgacggtccgcaggggagagcgccacccctcaggtgcataatgac 180
 |||||||
 Db 344 GCTATGACAAACGTGACGGTTCAGGAGGGGAGAGCGCCACCTCAGGTGCACAAATGAC 403
 QY 181 aaccggtcaccggtgtgctgtgttaaacccgacgacacatcctctatgtcgtggaatgac 240
 |||||||
 Db 404 AACCGAGTCACCCGGGTGGCTGCTGTAACCGCAGTACCATCTCTATGCTGGAATGAC 463
 QY 241 aagtggtgcctggtatcctcgcgtgtgtccttctgagcaacccaacgagtaacgac 300
 |||||||
 Db 464 AAGTGTGCTGCTAGATCTCTGCTGTGTCTCTGAGTAAACCCAGACCACTACAGCAT 523
 QY 301 gagatccagaacgtggtatgtatgacgagggcccttaacacctgctcgtgcagacagac 360
 |||||||
 Db 524 GAGATCCAGATGTGATGTGTATGATGAGGGCCCTTATACCTGCTCGGTACAGACAGAC 583
 QY 361 aaccacccaagaacctctaggtccacctaatgtgcagatattctcccaaatgtagag 420
 |||||||
 Db 584 AACCAACCTTAAGACCTCCAGGGTCCACCTCATTTGTACAAAGTATCTCCCAAAATTGNAGAG 643
 QY 421 attcttcagatatctccatlaatgaagggaacaatatagcctcactcgtgcatacgaact 480
 |||||||
 Db 644 ATTCTCTCANATATCTCTCATTAATGAAGGGAACAACATCAGCCTCATTGATAGCCACA 703
 QY 481 gtagaacagagccttaagcttcttgagacacatctctcccaagcggtgtgtg 540
 |||||||
 Db 704 GGTAGACCGAGCCTTACAGTAACCTGGANACATATTNT-CCAAGGCCGTTGGCTTGAG 762
 QY 541 agtga 545
 |||||||
 Db 763 AGTGA 767

RESULT 9
 BM009450 661 bp mRNA linear EST 30-OCT-2001
 LOCUS BM009450 603629962F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443743 5',
 DEFINITION mRNA sequence.
 ACCESSION BM009450
 VERSION BM009450.1 GI:16523804
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 661)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1921 row: 1 column: 16
High quality sequence stop: 659.

FEATURES
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1. .661
/organism="Homo sapiens"
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/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 190 a 175 c 171 g 125 t
ORIGIN

Query Match 44.8%; Score 462; DB 10; Length 661;
Best Local Similarity 93.9%; Pred. No. 3.6e-114;
Matches 505; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 528 ggttgcttgtgagtgaggaagaatacttggaattcagggcatcaccgggagcagtc 587
|||||
Db 1 GGTGGCTTGTGAGTGAAGACGAATACTTGAATTCAGGGCATCCCGGAGCAGTC 60
QY 588 aggggactacgagtgacgtgctcccaatgacgtgcccgcgcgtgtacggagagtaaa 647
|||||
Db 61 AGGGGACTACGAGTGACAGTGCAGTCCCAATGACGTGCCCGCCGTGTACGGAGACTAAA 120
QY 648 ggtcacctgaactatccacatacatctcagaagaagcgaaggtgtcccgctggg 707
|||||
Db 121 GGTCAACCGTGAACCTATCCACATTCATTCAGAGCCAAAGGCTACAGGTGTCCCGCTGGG 180
QY 708 acaaaagggacactgacgtgtgaagccctcagcagtcacccaattccagtgta 767
|||||
Db 181 ACAAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGATTCAGTGTGA 240
QY 768 caaggtgacaaaagactgattgaagaaagaggtgaagtggaagaaacagacctt 827
|||||
Db 241 CAAGGATGACAAAGACTGATGAAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 300
QY 828 cctctcaaaactcattcttcaatgtctctgaacatgactatggaactacacttgct 887
|||||
Db 301 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCT 360
QY 888 ggcctccaacaagctgggccaaccaatgccaagcatcatctattt----- 933
|||||
Db 361 GGCTCTCAACAAGCTGGGCCACCAATGCGCATGCTATTGTAAGTGAAACTAC 420
QY 934 -----ggtccaggcgccgtcagcgaggtgagcaagcgacgtgag 974
|||||
Db 421 AGCCCTGACCCCTTGGAAAGGTCCAGGGCGGTGAGCGAGGTGAGCAAGGGCAGCTGAG 480
QY 975 gaaggcaggtcgtctgtgctgctcctctctgtctgacactgctctcaattt 1032
|||||
Db 481 GAGGCGCAGGCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538

RESULT 10
BM423716 953 bp mRNA linear EST 29-JAN-2002
LOCUS BM423716

DEFINITION AGENCOURT_6398987 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5516929
5', mRNA sequence.
ACCESSION BM423716
VERSION BM423716.1 GI:18391928
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 953)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2018 row: f column: 02
High quality sequence start: 10
High quality sequence stop: 571.
High quality sequence stop: 571.

FEATURES
source

1. .953
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5516929"
/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 278 a 211 c 256 g 201 t 7 others
ORIGIN

Query Match 44.8%; Score 462; DB 10; Length 953;
Best Local Similarity 93.9%; Pred. No. 4.4e-114;
Matches 505; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 528 ggttgcttgtgagtgaggaagaatacttggaattcagggcatcaccgggagcagtc 587
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Db 26 GGTGGCTTGTGAGTGAAGACGAATACTTGAATTCAGGGCATCCCGGAGCAGTC 85
QY 588 aggggactacgagtgacgtgctcccaatgacgtgcccgcgcgtgtacggagagtaaa 647
|||||
Db 86 AGGGGACTACGAGTGACAGTGCAGTCCCAATGACGTGCCCGCGGTGTACGGAGACTAAA 145
QY 648 ggtcacctgaactatccacatacatctcagaagcgaaggtgtacaggtgtcccgctggg 707
|||||
Db 146 GGTCAACCGTGAACCTATCCACATTCATTCAGAGCCAAAGGTACAGGTGTCCCGTGGG 205
QY 708 acaaaagggacactgacgtgtgaagccctcagcagtcacccaattccagtgta 767
|||||
Db 206 ACAAAAGGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGATTCAGTGTGA 265
QY 768 caaggtgacaaaagactgattgaagaaagaggtgaagtggaagaaacagaccttt 827
|||||
Db 266 CAAGGATGACAAAGACTGATGAAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 325
QY 828 cctctcaaaactcattcttcaatgtctctgaacatgactatggaactacacttgct 887
|||||
Db 326 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAGACTACACTTGGCT 385

[illegible]

RESULT	11
BEO14142	
LOCUS	BEO14142
DEFINITION	125737 MARC 1P1G Sus scrofa cDNA 5' , mRNA linear EST 09-JUL-2000
ACCESSION	BEO14142
VERSION	BEO14142.1
KEYWORDS	GI:8275136
EST.	
SOURCE	pig.

REFERENCE
AUTHORS
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
1 (bases 1 to 524)
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA

Email: smith@email.marc.usda.gov
Fax: 402 / 62 4390
Single pass sequencing. Bases called and alt_trimmed with phred
V0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

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PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 53   row: G   column: 8
Seq primer: ATTTAGGTGACACACTATAG.
Location/Qualifiers
1. .524
FEATURES
source
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

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Query Match	44.3%;	Score 457.4;	DB 9;	Length 524;
Best Local Similarity	92.2%;	Pred. No. 5.7e-113;		
Matches 482;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;

QY 170 gcaatttgacaacccgggtcacccggtgacctgctgaacccgcagcaccatcctcatg 229
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 GCACGATGCACAACC GGGTCA CCGGGTGGCTGGCTAACC GAAGCACCATCCTCTATTG 61

QY 230 ctggyaatgacaagtgtgtgacctgatccttcgctgtgtccttctgagcaaacaccaaacgc 289
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CGGGGAATGACAAGTGTGTGCTTGACCCCGCGTGGTCTGCTTAGCAACACCCAGACCC 121

QY 290 agtacagcatcgatccagaacgtgtatgttatgacgagggcccttaacactgtccg 349
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	122	AGTACAGCATCGAGATCCAGAAATGTGGACGCTGTACGACGAGGGGCCGTACACCGTCTCTG	181
QY	350	tgcgaacacagacaaccacccaagaagaccttaaggtccacctcatattgtgcaagtatctocca	409
Db	182	TGCAGACAGACACACCACCCCAAGACCTCCCGGGTCCACCTCATTTGTGCAAGTATCTCCCA	241
QY	410	aaattgttagagattctctcagatatctccatlaatgaagygaaacaatatatagcctcacct	469
Db	242	AAATTGTAGAGATTTCTTCAGATATCTCCATTAAAGCAAGGGAACAATATCAGCCTCACCT	301
QY	470	gcatagcgaactggtagtaaccagagaccctaogtltacttggagacacatctctcccaagcgy	529
Db	302	GCAATAGCAACAGGTAGACCCAGAGCCTACGGTGAACCTGGAGACACATCTCCCCAAAAGCTG	361
QY	530	ttggtcttgtgagtgaagaacgaatacttggaaaltcaggygcatacccggyagcagttcag	589
Db	362	TGGGCTTTGTGAGTGAAGATGAATACTTGGAGATCCAGGGGCATCACACGGAGCAGTCAAG	421
QY	590	gggactacgagttgcagtgccctccaatgaacgtggccgcgcccgtggtacggaagataaagy	649
Db	422	GGGACTACGAGTGCAGGCGCCTCCAAATGAACGTGGCTGCTCCGGTGGTGGCGGAGAGTCAAGG	481
QY	650	tcaccgtgaactatccacacatacatattcagaagaagccaaggytac	692
Db	482	TCACCGTGAACATACTCCCATATACATTTCAGAAAGCTAAGGGGCAC	524

RESULT	12
LOCUS	602373361F1
DEFINITION	mus musculus CDNA clone IMAGE:4480983 5'
ACCESSION	BG261691
VERSION	BG261691.1

SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
1 (bases 1 to 979)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaphs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM10315 row: 1 column: 16
High quality sequence stop: 715.

FEATURES	Source
Location/Qualifiers	1. .979
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/tissue_type="retina"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	
BASE COUNT	231 a 261 c 289 g 198 t
ORIGIN	

Query Match	44.1%;	Score 455;	DB 10;	Length 979;
Best Local Similarity	86.3%;	Pred. No. 3.5e-112;		

Matches 562; Conservative 0; Mismatches 80; Indels 9; Gaps 5;

```
QY 81 aggaagtcgcccgtgcgacgagatgacacccctcccaaaagtatgacacagtcagct 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 AGGAGTGCCTGCGTAGGAGATGCCACCTTCCCAAAGCTATGACCAACGTCACGGT 182

QY 141 ccggcaggggagagcgccacccctcagtgcaactattgacaaacgggtcaaccgggtg 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 CAGGACAGGGGAGAGAGCGCCACCCCTCAGTGCACATGACACACCGAGTCACCCGGGTGGC 242

QY 201 ctggttaaacccgacgacacatcctctatgctggaatgacaaagtgtgctgtatcctcg 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 CTGGCTAAACCGCAGTACCATCTCTATGCTGGAATGACAAAGTGTGCTAGATCTCG 302

QY 261 cgtgtcctcttgagcaacacccaaacgagtlacagcatcgagatccagaaagtgatgt 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 TGTGTCCTCTGAGTAACACCCAGACCCAGTACAGCATGAGATCCAGATGAGATGT 362

QY 321 gtagcagagggcccttacacctgtcgtgagacagacacaccccaaaagaccttag 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 363 GTACGATGAGGGCCCTTATACCTGTCTGGTACAGACAGACCAACCCCTTAAGACCTCCA- 421

QY 381 ggtcacctcatgtgcaagatctcccaaatgtgagatctctcagatattccat 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 GGTCCACCTCATTTGACAGATCTCCCAAATTTGAGAGATTTCTTCAGATATCTCAT 481

QY 441 taatgaaggaacaatatatgaacctgaacctgacactgtagaccagagcctacgt 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 TAATGAAGGGAACAACATCAGCCTCAGTGCATAGCCACAGTAGACCGGAGCCTACAGT 541

QY 501 tacttgagacacatctctcccaaacgggttgcttgtgtgagtgaaagcgaatacttga 560
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 AACCTGGAGACATATTCTTCCCAAGGCCGTTGGCTTTGTGAGTAGAGATGAGTTCCCTGGA 601

QY 561 aattcagggcatcacccgggagagcagtcaggggactacagagtcagtcctccaatgacgt 620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 GATCCAGGACATCACTCGGGAACAGTCAAGCGAGTACGAGTGCAGCGC--TCAACGACGT 659

QY 621 ggcgcgcccgtgtacgagagtaaaagtcaacgtgaactatccacatatactcaga 680
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 660 GGC--GGACCGTGTGACGAGAGTGAAGGTG--CCGTGAATATACCATATCATTTCTAGA 716

QY 681 agccaaggtlacagtgcccccggtgggacaaaaggggacactgcaagtgtga 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 AGTTAAGG--CCCGGTGTCCCGTGGGGGAGAGGGGCTCTGACAGTGTGA 764
```

RESULT 13
BI755360 849 bp mRNA linear EST 25-SEP-2001

LOCUS 603024964F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195750 5',
DEFINITION mRNA sequence.

ACCESSION BI755360
VERSION BI755360.1 GI:15746938

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 849)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM11489 row: 0 column: 15

High quality sequence stop: 848.

FEATURES
source location/Qualifiers

1..849

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5195750"

/clone_lib="NIH_MGC_114"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research and Genetics tracking code 019. Note:

this is a NIH_MGC Library."

BASE COUNT 218 a 239 c 227 g 165 t
ORIGIN

Query Match 43.6%; Score 450; DB 10; Length 849;

Best Local Similarity 76.4%; Pred. No. 7.4e-111;

Matches 579; Conservative 0; Mismatches 175; Indels 4; Gaps 2;

```
QY 20 aaatgacaattctatctcttggcaactctcaggggctgctgtctctctcc 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 AGATGACCATCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143

QY 80 aagagtgcccgtgcgacgagatgcaactcccaaaagtatgacacagtcagc 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 CAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAAGCTATGACCAACGTCACGG 203

QY 140 tccgagggggagagcgccacccctcagtgacattgacaacgggtcacccgggtg 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 TCCGGCAGGGGAGAGAGCGGCCACCTCAGGTGATACCATAGATGACCGGGTAAACCGGGTGG 263

QY 200 cctgtctaaccgcagcacacatctctatgtctgggaatgacaagtgtgtcctgatactc 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 CCTGGCTAAACCGACGACCATCTCTTACGCTGGGAATGACAAGTGTCCATAGACCTC 323

QY 260 gcgtgtcctcttgagcaacacccaaacgagtlacagcatcgagatccagaacgtgatg 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 GTGTGATCATCTCTGTCAATPACACCAACCCAGTACAGCATCATGATCCAAATGTGATG 383

QY 320 tgtatgacgagggcccttaaacactgtcgtgtgacagacagaaacccaagaactcta 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 TGTATGACGAGAGGTCCGTAACCTGTCTGTGACAGACAGACAATCATCTCCAAACGTCCTC 443

QY 380 gggtcacacatctgtgcaaglatctcccaaatgtgagatcttctcagatattcca 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 444 GGGTTACCTAATAGTGAAGTTCCTCTCAGATCATGAATATCTCTCAGACATCACTG 503

QY 440 ttaatgaaggaacaatatatgaacctgaacctgacactgtagaccagagcctacg 499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 504 TGAATGAGGGAAGCAGTGTGACCCCTGTGTGTCTTGTATTTGGACAGACAGACCAACTG 563

QY 500 ttacttgagacacatctctccca--aagcggttgcttgtgtgtaagaacgaatcact 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 564 TGACATGAGGACACCTGTCAATCAACGAGGCCAGGCTTTGTAGTACAGGATGAGTAC 623

QY 557 tggaaattcagggcatcacccgggagcagtcaggggactaagatgagtcagtcctccaatg 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 624 TGGAGATCTTGAACATCAAGCGAGACCATCTCCGGGAGTACGAATGACGCCCTTGAACG 683

QY 617 acgtggcggcccgtgtgacgagagt--aaagtcaacgctgaactatccacataact 675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 684 ATGTGCTGCGCCCGATGTGCGGAAGTCACAAAATCACTGTCAACTATCTCCCTATATC 743

QY 676 tcagaagccaaggttacaggtgtcccggtgggacaaaaggggacacatgagtcagtcgagcc 735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 744 TCAAAAGCCAAAGAACACATGCTGTTCAGTCCGGCAGAGGGCATCTGTAGCTGTGAAGCC 803
```


size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 194 a 164 c 148 g 127 t
ORIGIN

Query Match 41.0%; Score 423.2; DB 10; Length 633;
Best Local Similarity 98.9%; Pred. No. 1.1e-103;
Matches 447; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 atgaaaccatccagccaaaatgacaaattctatctcttggcaatcttcacgggctg 60
DB 183 ATGAAACCATCCAGCCAAAATGACAAATCTATCTCTTGGCAATCTCAGGGGCTG 242
QY 61 gctgctctgtctcttccaaaggagtgccgtgcgcaaggagatgcaccttcccaaa 120
DB 243 GCTGCTGTGTCTCTTCCAAAGAGATGCCGTGCCAGCGGAGATGCCACCTTCCCAAA 302
QY 121 gctatggacaacgtgacggtccggcaggaggagagccaccctcagtgacattgac 180
DB 303 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGGCCACCTCAGGTGACATTTGAC 362
QY 181 aaccgggtcaccocgggtggcctggtctaaaccgcagcaccatcctctatgtggaatgac 240
DB 363 AACGGGTACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 422
QY 241 aagtgtgctggtgatcctcgcgtgtgtccttcttgagcaaacacccaacgcagtaacagcatc 300
DB 423 AAGTGTGCTGGATCCTTCGGGTGGTCTTCTGAGCAACA-CCAAACGAGTACAGCATC 481
QY 301 gagatccagaacgtgagatgtatgacgaggggcccttaacacctgctcgtgcagacagac 360
DB 482 GAGATCCAGAACGTGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 541
QY 361 aaccacccaaagacctctaggggtccacctcaattgtcaagtatctcccaaat-tgtaga 419
DB 542 AAACAACCAAGACCTTACGGGTCCACCTCATTTGCAAGTAICTCCCAAAATAGGTAGA 601
QY 420 gatttctcagatatctccatlaatgaaggga 451
DB 602 GATTCTTCAGATATCTCCATTAATGAAGGGA 633

Search completed: July 11, 2002, 21:28:00
Job time: 10359 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2002, 22:51:36 ; Search time 4995.85 Seconds

(without alignments)
7091.611 Million cell updates/sec

Title: US-09-700-397-2
Perfect score: 1693
Sequence: 1 gtccttcagcaaaacagtgg.....aaaaaaaaaaaaaaaaaaaa 1693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	1440.2	85.1	1839	9	AF126426	AF126426 Homo sapi
2	1002.2	59.2	2040	10	RNU16845	U16845 Rattus norv
3	912.2	53.9	1410	10	AF282980	AF282980 Mus muscu
4	643.8	38.0	1058	5	AF292935	AF292935 Gallus ga
5	641.8	37.9	1257	5	GGCEPU1	Z72497 G.gallus mr
6	638.2	37.7	1035	5	AB011810	AB011810 Gallus ga
7	623.6	36.8	1638	12	AF271233	AF271233 Synthetic
c 8	619.8	36.6	190864	2	AP004248	AP004248 Homo sapi
c 9	618.2	36.5	202505	2	AP000912	AP000912 Homo sapi
c 10	616.6	36.4	184716	2	AC018368	AC018368 Homo sapi
11	604.8	35.7	1013	5	AF292936	AF292936 Gallus ga
12	603.8	35.7	187203	2	AP000832	AP000832 Homo sapi
13	571.2	33.7	1533	5	FFNINH55A	Y08170 Gallus gall
14	571.8	32.6	1556	5	AF292934	AF292934 Gallus ga
15	545.4	32.2	2593	4	BTOBCAM	X12672 Bovine mRNA
16	540.8	31.9	3069	10	RATCALMA	M88709 Rattus norv
17	539.2	31.8	1478	9	HUMOBGAM	L34774 Human (clon
18	523	30.9	2179	10	RATCALMB	M88710 Rattus norv
19	523	30.9	2337	10	RATCALMC	M88711 Rattus norv
20	465.2	27.5	2935	12	AF271618	AF271618 Synthetic
21	465.2	27.5	3216	5	GGCEPUS	AJ225897 Gallus ga
22	435.4	25.7	756	12	AF271232	AF271232 Synthetic
23	430.2	25.4	452	6	AX079423	AX079423 Sequence
24	362	21.4	1107	5	GGIAMPG9	Z94718 G.gallus mr
25	359.2	21.2	1158	5	GGIAMPG19	Z94720 G.gallus mr
26	357.6	21.1	2050	5	GGI19SPRO	Y08171 Gallus gall
27	348.4	20.6	1194	5	GGIAMPG11	Z94719 G.gallus mr
28	343	20.3	1238	6	AR030575	AR030575 Sequence
29	343	20.3	1238	10	RNU31554	U31554 Rattus norv
30	340.6	20.1	924	6	AR030579	AR030579 Sequence
31	340.6	20.1	977	6	AR030574	AR030574 Sequence
32	340.6	20.1	1014	6	AR030577	AR030577 Sequence
33	340.6	20.1	1017	9	HSU41901	U41901 Human limb
34	338.6	20.0	861	6	AR030581	AR030581 Sequence
35	338.6	20.0	912	6	AR030578	AR030578 Sequence
36	337.4	19.9	945	6	AR030580	AR030580 Sequence
37	333.8	19.7	861	6	AR030582	AR030582 Sequence
38	303.6	17.9	756	6	AR030589	AR030589 Sequence
39	298.2	17.6	756	6	AR030590	AR030590 Sequence
40	280.4	16.6	1059	5	GGAI32999	AJ132999 Gallus Ga
41	279	16.5	1809	10	AB017139	AB017139 Rattus no
c 42	256	15.1	257	11	G07361	G07361 human STS W
c 43	238.4	14.1	42263	2	AP004721	AP004721 Homo sapi
c 44	235.6	13.9	203572	9	AC016769	AC016769 Homo sapi
c 45	209.4	12.4	152686	2	AC018913	AC018913 Homo sapi

ALIGNMENTS

RESULT 1	AF126426	1839 bp	mRNA	linear	PRI 06-MAR-2000
LOCUS	AF126426				
DEFINITION	Homo sapiens neurotrimin (HNT) mRNA, complete cds.				
ACCESSION	AF126426				
VERSION	AF126426.1	GI:7158997			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1839)
AUTHORS Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE Cloning and identification of human neurotrimin full length cDNA

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1839)
AUTHORS Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE Direct Submission

JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES
source location/Qualifiers
1. 1839
/organism="Homo sapiens"

/db_xref="taxon:9606"
1. .1839
/gene="HNT"
265. .1299
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/note="similar to Rattus norvegicus neurotrinin"
/codon_start=1
/product="neurotrinin"
/protein_id="AAF37591.1"
/db_xref="GI:7158998"
/translation="MGVCGYLFPLPMKLVVSLRLFLVPTGVPVRSGDATFPKAMDN
VYVRQGESATLRCTIDNRVTRVAMLNRSTILYAGNDKWLDPVLLSNTQTQSYIEI
QNVVYDEGPTQSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCLAE
GRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGDYECASNDVAPVVRKVT
VNPEPYISEAKGTVPGVKQLQCEASAVPSAEFQWYKDKRLIEGKGVKVENRPF
LSKLIFNVSEHIDYGNVTCVSNKLGHTNASIMLFGPGLVSEVSNIGTSRRGCVWLLP
LVLHLLKLF"

BASE COUNT 464 a 506 c 503 g 366 t
ORIGIN

Query Match 85.1%; Score 1440.2; DB 9; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 3; Indels 20; Gaps 1;

QY 210 aggaatgccccgtgacagcgagagatgccacctccccaagaatgtgacacagtgacgt 269
Db 345 AGGAGTGGCCCTGGCGAGCGGAGATGCCACCTTCCCAAAGCTATGACACAGTGACGCT 404
QY 270 ccgacgagggagagagcgccacccctcagtgacatattgacacacgggtgcacccgggtgc 329
Db 405 CCGGACGGGGGAGAGCGCCACCTCAGGTGACACTATTGACACCGGGGTACCCCGGGTGGC 464
QY 330 ctggttaaacgcagacacatcctctatgtcgtggaatgacaaagtgtgcctggatcctcg 389
Db 465 CTGGCTTAAACCGGACACCATCTCTATGCTGGGAATGACAAAGTGGTCCCTGGATCCTCG 524
QY 390 cgtgtcctctgagcaacacccaaacgagtaacagatcgaagatccagaacgttgatgt 449
Db 525 CGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAACGTGGATGT 584
QY 450 gtagacagggcccttaacacgtcgtgtagacagacagacacacacacacacacacacac 509
Db 585 GTATGACGAGGGCCCTTACACCTGCTGCGGTGACAGACAGACACACACCAAGACCTTAG 644
QY 510 ggtcacctcatgtgcaagtatctcccaaatgttagagattcttcagatatccat 569
Db 645 GGTCCACCTCATGTGCAAGTATCTCCCAAATGTAGAGATTCTTCAGATATCTCCAT 704
QY 570 taatgaagggaacatatagcctcagtcagtaactgttagacacagacacacacacacac 629
Db 705 TAATGAAGGGAACAATATTAGCCTCAGCTGCATACCAACTGTGTAGACACAGACCTTAG 764
QY 630 tacttgagacacatctctcccaaacggttgcttgtgagtgaagacgaatacttga 689
Db 765 TACTTGAGACACATCTCTCCCAAAGGGGTGGCTTTGTGAGTGAAGACGAATACTTGA 824
QY 690 aattcagggcatcaccgggagcagtgagtgactagagtgacgtgcctccatgacgt 749
Db 825 AATTCAAGGGCATCACCCGGGAACAGTACAGGACTACGAGTGCAGTGCCTCCCATGACGT 884
QY 750 ggcgcgcgcgtgtgtagcggagagtaaggtcacacgtgaactatccacacacacacacac 809
Db 885 GGC CGCGCGCGCTGTGTAGGAGAGTAAGGTCAACCGTGAACCTATCCACCATATTTCAGA 944
QY 810 agccaaggtlacaggttccccgttgagacaaaagggagacactgacgtgtgaagcctcagc 869
Db 945 AGCCAAGGTTACAGGTGCCCGGTGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004
QY 870 agtccccctcagcagaatccagtgtagacaagatgacaaagacgtatgaagaaagaa 929
Db 1005 AGTCCCTCAGCAGAATTCAGTGTGTACAAAGATGACAAAAGACGTGATGAAGAAAGAA 1064

QY 930 aggggtgaagtggaaacacagaccttctctcacaactcatctctcgaatgtctctga 989
Db 1065 AGGGGTGAAGTGAAGAAACAGACACCTTCTCTCAAAACTCATCTCTTCATATGTCTCTGA 1124
QY 990 acatgactatggaaactacacttgcgttggtcctccaacagctgggccaacacacacac 1049
Db 1125 ACATGACTATGGGAACACTACACTTGCCTGCTCCCAACAGCTGGGCCACCAATGCCAG 1184
QY 1050 catcatgtatttggccagcgccgtcagcgagtgagcaacgacgacgtcgagagggc 1109
Db 1185 CATCATGTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGCAACGGCACGTGAGAGGCGC 1244
QY 1110 aggtcgtctgtgctgtcgtcctctctgtgtcttgacacgtctcacaatttgatgta 1169
Db 1245 AGGTCGCTGTGGCTGCTGCTCTCTGTGCTTGACACCTGCTTCAATTTTGATGTGA 1304
QY 1170 gtgcacactcccccacccgggaaagctgcgcgcacacacacacacacacacacac 1229
Db 1305 GTGCCACTTCCCAACCCGGGAAGGCTGCCGCCACACCAACCAACACAGCAATG 1364
QY 1230 gcaacacccgacagcaacacacacacacacacacacacacacacacacacacac 1289
Db 1365 GCAACACCCGACAGCAACCAATCAGATATATCAAAATGAAATAGAAAGAACACAGCCCTCA 1424
QY 1290 tgggacagaaatttgaaggagggagaaacaaagaaacttggggggaaagaaagttttaa 1349
Db 1425 TGGGACAGAAATTTGAGGGAGGGGAAACAAGAAATACTTTGGGGGGAAGAGCTTTTAA 1484
QY 1350 aagaatltgaatltgccttgagatatattagtlacaaatgagtttcttcccaacg 1409
Db 1485 AAGAAATTTGAAATTTGCCCTTGAGATATTTAGGTACAAATGAGATTTCTTTCCCAACG 1544
QY 1410 ggaagaacacagacaccccgcttgacacacacacacacacacacacacacacacac 1469
Db 1545 GGAAGAACACAGACACACCCGCTTGAGACCACTGCAAGCTGCATCGTGAACCTCTTGG 1604
QY 1470 tgcacgtgtggcgaagggtcagcctctctgcccacagagtgccccacgttgaacatc 1529
Db 1605 TGCCAGTGTGGGCAAGGGCTACGCTCTCTGCCACAGACTGCCCCACAGTGAACATTC 1664
QY 1530 tggagcttggccatcccaatcattcagtcagtagagacgaacagaaatgagac----- 1582
Db 1665 TGGAGCTGGCCATCCCAATTCATCAGTCCATAGAGACGAACGAATGAGACCTTCCG 1724
QY 1583 -----cttcgggcccaagcgtgcgcctgcgggcacttggtagactgtgcca 1629
Db 1725 CCCAAGCGTGGCGCTTCCGCGCCCAAGCGTGGCGCTGCGGCGCACTTGGTAGACTGTGCCA 1784
QY 1630 ccaagcgctgtgtgtgaacgtgaataaaaaagacaaaaaagaaaaa 1684
Db 1785 CCACGGCGTGTGTGTGAACGTGAATAAAGAACCAAAAAA 1839

RESULT 2
LOCUS RNUI6845 2040 bp mRNA linear ROD 26-MAY-1995
DEFINITION Rattus norvegicus neurotrinin mRNA, complete cds.
ACCESSION U16845
VERSION U16845.1 GI:755184
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
and Salzer,J.L.
TITLE Cloning of neurotrinin defines a new subfamily of differentially
expressed neural cell adhesion molecules
JOURNAL J. Neurosci. 15 (3), 2141-2156 (1995)
MEDLINE 95198094
REFERENCE 2 (bases 1 to 2040)

AUTHORS Salzer, J.L.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical Center, 550 First Avenue, New York, NY 10016, USA

FEATURES

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1. 2040
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
484. .1518
/note="neural cell adhesion molecule"
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/translation="MGVCGYLFLEPWKLVVVSRLFLVPTGVPRSGDAEPKAMDNVTROGESATLRCTIDNRVTRVAMLNRSITLYAGNDKWLDPVLLSNQTSIEIQNDVYDEGPYTCVQTDNPKTSRVHLIVQVSPKIVEIS...ISINEGNISLTICATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGEYECASNDVAAPVVRVNTVNPPISEAKGTGVPVGQKGTLOCEASAVPSAEFQWFKDKRLVEGKKGVKVENRPLSRLTFPNVSEHDYGVNTCVASNKLGHNTASIMLFPGAVSFVNNGTSRRAGCIMLLPLVHLHLIKF"

BASE COUNT 504 a 544 c 551 g 441 t
ORIGIN

Query Match 59.2%; Score 1002.2; DB 10; Length 2040;
Best Local Similarity 84.6%; Pred. NO. 4.3e-244;
Matches 1262; Conservative 0; Mismatches 198; Indels 31; Gaps 11;

QY 210 aggaatgcccgctgcgcagcggagatgacacccctccccaagctatgagacaacgtgacgt 269
DB 564 AGGAGTCCCGGTGCGTACCGGAGATGCCACCTTCCCAAAGCTATGGACACACGTGACGGT 623
QY 270 ccggcaggggagagagcgccacccctcaggtgcatctatgacaaccgggtgcacccgggtgc 329
DB 624 CAGGCAGGGGAGAGCGCCACCTCAGGTGCACAAATTGACAAACCCGAGTCAACCCGGGTGGC 683
QY 330 ctggctaaccgcagcacccatcctctatgctgggaatgacaagtgtgctgtgacccctcg 389
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QY 630 tacttgagagacacatctctcccaagcggttgcttgtgagtgaagaacgaatacttga 689
DB 984 AACCTGGAGACATATTTCTCCCAAAGCTGTGGCTTTGTGAGTGAGAGTACCTGGA 1043
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QY 990 acatgactatgggaactacacttgcgtgtgcctccaacagctgggccaaccaatggcag 1049
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QY 1515 ccacgtggaacattctgtgagcttgcacatcccaattcaatcagttcatagagac--gaac 1572
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QY 1573 agaatgagacctccggcccaagcggtgcgtgcgtgcacatttgttagactgtgtccacca 1632
DB 1930 AGAGTGAGAAACAGGGGCCCAAGAGTGCACAGGAGGCCCTTTGGTGGGCTGCGCGCATGG 1989
QY 1633 cggcgtgtgtgtgaacgtgaataaaaaagagcaaaaaaagagagagagagagagagag 1683
DB 1990 TGGCGTGTGTGATGAAGTGTGAATCCGAAGTAGAAAAAACAAGATTA 2040

RESULT 3

AF282980 1410 bp mRNA linear ROD 01-FEB-2001

LOCUS AF282980 Mus musculus neurotrophin mRNA, complete cds.

DEFINITION AF282980 Mus musculus neurotrophin mRNA, complete cds.

ACCESSION AF282980

VERSION AF282980.1 GI:12642539

KEYWORDS house mouse.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1410)

AUTHORS Kim, T.H., Choi, S.C., Kim, J., Jeon, J.W., Kim, K.D. and Lee, S.H.

TITLE Cloning and expression of mouse neurotrophin gene in the developing nervous system

TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The University of Liverpool, Ashton Street, Liverpool, Merseyside L69 3GE, UK

FEATURES
source

Location/Qualifiers
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/tissue_type="brain"
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52..993
/gene="CEPU-Se"
/note="IgION family protein; secreted form of CEPU-1"
/codon_start=1
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/protein_id="AA01878.1"
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/translation="MAQAKMHPVSWVIFAGMAALLFQGVPRSGDAFPKAMNVT
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BASE COUNT 250 a 320 c 310 g 178 t
ORIGIN

Query Match 38.0%; Score 643.8; DB 5; Length 1058;
Best Local Similarity 79.5%; Pred. No. 6.5e-153;
Matches 762; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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DB 23 GAAGGAGGGGAGGACACGACCTCCGAATATGGCCAGCGAAATGCACACCCCGCT 82
QY 167 ctgggcaatcttcacggggtgctgtctgtctcttccaagagtgccctgtgcga 226
DB 83 CATGGGTGATCTTCGCCGGGAGATGGCCGACCTCCTCTCCAAAGAGAGCCCGTGGCA 142
QY 227 gcggagatgccccttccccaaagctatgtgacaacgtgacggtccggcaggggagagcg 286
DB 143 GCGGAGATGCCACCTTCCCAAGCTATGACACAGTGACTGTGCGCGACAGGGAGAGTG 202
QY 287 ccaccctcagtgcaactatgaacaaaccgggtcaaccgggtgctgtcctaaaccgcagca 346
DB 203 CCACGCTCAGGTGCTCCGTGGAACACCGCGCTCACCCGCTGGCTGAACCCGACGA 262
QY 347 ccaccctcctatgtggaatgacaagtgtgctgtgacccctgcgtgtcctcttgagca 406
DB 263 GCATCCTCTATGCCGCAATGACAAGTGTGTGACCCGAGGGGTGTCTCTCTGCCA 322
QY 407 acacccaacgcagtacagcatcgagatccagaaacgtgacgtgtatgacaggccctt 466
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QY 467 acaccgtctggtgcagacagacaaccacaaagacctaggtccacctatgtgc 526
DB 383 ACACCTGCTCCGTGCAGACAGACATCACCCCAAGACATCTGCGGTGCACCTCATTTGTC 442
QY 527 aagtatctcccaaaattgttagagattcttcagatatctccattaatgaagggaacata 586
DB 443 AAGTGTCCGGAATTTACCGAGATCTCTCTGACATCTCCATCAATGAAGTGGCAACG 502
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DB 503 TCAGCCTCACTGCTAGCCACAGGCGACAGCCCAACCAATCACTGAGACACATCT 562
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QY 707 gggagcagtcaggagactacgagtgcagtcctccaatgcagctggtccgcccgtgtac 766
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QY 767 ggagagtaaggtcacccgtgaactatccaccatattccaagaagccaaggtacagtg 826
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QY 827 tcccggtggacaagaaggagacactgagtgtagaacctcagcagtcctccctcagcagaat 886
DB 743 TGCCGCTGGGCGAGAGGCGATCTGATGTGTAAGCCTCCGCTGTGCCCTGTCTGACT 802
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DB 803 TCCAGTGTACAAGACGACACAGCGGCTGGCTGAAGACAGAAAGGCTGAAGGTGGA 862
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QY 1007 aaactgctggtccctccaacaagctgggccaaccaatgccagatcatgtatttgt 1065
DB 923 ACACCTGCGTGGCTCCCAACGACTGAGAAACACCAACGCCAGCATGATCTTTATGT 981

RESULT 5
GCEPU1 1257 bp mRNA linear VRT 29-APR-1998
LOCUS GCEPU1
DEFINITION G.gallus mRNA for CEPU-1.
ACCESSION Z72497
VERSION Z72497.1 GI:1325950
KEYWORDS Brain; CEPU-1; glycoprotein; GPI-anchor protein.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 1257)
AUTHORS Spaltman, F. and Brummendorf, T.
TITLE CEPU-1, a novel immunoglobulin superfamily molecule, is expressed
by developing cerebellar Purkinje cells
JOURNAL J. Neurosci. 16 (5), 1770-1779 (1996)
MEDLINE 96370549
REFERENCE 2 (bases 1 to 1257)
AUTHORS Brummendorf, T.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1996) Brummendorf T., Max-Planck-Institute for
Developmental Biology, Molecular Biology, Spemannstrasse 35,
Tuebingen, Germany, 72076

FEATURES
source

Location/Qualifiers
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/clone="KB17"
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Db	441	CAATGAAGGTGGCAACGTACGCTCACCCTGATAGCCACGGGACGCCACAGACCCACAAT	500
QY	630	tacttgagacacatctctcccaagcgglttgcttgttagtgaagacyaatacttga	689
Db	501	CACCTGGAGACACATCTCGCCCAAAGCTGTGGCTTCATCAGCGAGGACGAGTACCTGGA	560
QY	690	aattcagggcatcaccggagcagtcaggggagtaaggtcacccgtgaactatccacatacttcaga	749
Db	561	GATTCACAGCATCACGAGGAGCAGTCGGGCGAGTACGAGTGCAGTGCCTCCACGACGCT	620
QY	750	ggccgagcccggtgtacgagagtaaggtcacccgtgaactatccacatacttcaga	809
Db	621	GGCCGGCGCTGTGCTCCAGCGAGTCAAAAGTCAACCTACCCACCGTACATCTCGGA	680
QY	810	agccaaggttacaggtgtccccggtgaggaacaaaggagcactgcaggtgtgaagcctcagc	869
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QY	930	agggggtgaagtggaaacagacccttcctctcaaaactcatctctcaatgtctgtga	989
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QY	990	acatgaactatgggaactacacttgcgtgscctccaacagctyggccacacccaatgccag	1049
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QY	1050	catcatgtctattgtgtccagggccgttcagcagaggtgagcaacgagcgtcgaggggc	1109
Db	921	CATGATCCTTTATGGCCCCCGGTGCAGTGCAGGATGGCAACAGCGGTGCGTGGCGGAGG	980
QY	1110	aggtcgcgtctgctgtcctcttctgttcttgacactgtccttctcaatttga	1164
Db	981	CAGCTGTGCTGTGCTGTGGCCCTGCGCTGCCCAAGCTGCCCGCAGTCTCTGA	1035
RESULT 7			
AF271233			
LOCUS	AF271233	1638 bp	DNA linear SYN 21-MAY-2001
DEFINITION	Synthetic construct secretory IgCEPUS-GFP fusion protein (IgCEPUS-GFP) gene, complete cds.		
ACCESSION	AF271233		
VERSION	AF271233.1 GI:14161268		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 1638)		
AUTHORS	Kim,D.-S. and Moss,D.J.		
TITLE	Secretory IgCEPUS-GFP fusion protein expressions in transfected cell lines		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1638)		
AUTHORS	Kim,D.-S. and Moss,D.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-MAY-2000) College of Natural Resources and Life Science, Division of Biological Resources R-6517, Dong-A University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of Korea		
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BASE COUNT	386 a 533 c 460 g 259 t	
ORIGIN		
Query Match	36.8%; Score 623.6; DB 12; Length 1638;	
Best Local Similarity	80.0%; Pred. No. 9.8e-148;	
Matches 734; Conservative	0; Mismatches 184; Indels 0; Gaps 0;	
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QY	201 tctctccaaggagtgcccggtgcgcagcggagatgcacacttcccaagctatgacaa	260
Db	66 CCTCTTCCAAGAGATGCCCGTGGCAGCGGAGATGCCACCTTCCCAAAGCTATGACAA	125
QY	261 cgtgacggtccggcaggggagagcgccacccctcaggtgtcactatlgacaacccgggtcac	320
Db	126 CGTGACTGTGGCGGCAAGGGAGAGTGGCCACGCTCAGGTGCTCCGTGACAAACCGGTCAC	185
QY	321 ccgggtgacctggttaaacccgagcaccatcctctatctgtggaatgacaagtgtgct	380
Db	186 CCGCGTGGCTGTGCTGAACCGCAGCAGCATCTCTATGCCGGCAATGACAAAGTGTGCTT	245
QY	381 ggatcctcggtgtgtcctcttgagcaacacccaacgagtlacagctcagatccagaa	440
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QY	441 cgtgatgtgtatgacagggcccttacacctgtcgtgtgcagacagacaacccaacaa	500
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QY	501 gacctctaggttccacctcatctgtgcaagtatctcccaaatgttagagattcttcaga	560
Db	366 GACATCTCGCGTGACCTCATTTGTGCAAGTGTGCCGAAATTAACCGAGATCTTCTGA	425
QY	561 tatctccatgaaggaacaatatattagcctcacctgcatagcaactggttagaccaga	620
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QY	621 gctcaggttacttgagacacatctctccaaagcgttggtcttgttagtgaagaca	680
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QY	681 ataacttgaaattcaaggcatcacccgggagcagtcaggggactacgagtgagtgctc	740
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QY	741 caatgacgtggccggtgtgtacgagagtaaggtcacccgtgaactatccaccata	800
Db	606 CAACGACGTGGCGCGCTGTGCTCCAGCGAGTCAAAAGTCAACCGTCAACTACCAACCGTA	665
QY	801 catttcaggaagccaagggtacaggtgtcccggtggacaagaaggagacactgcagtgta	860

Db 666 CATCTCGATCGAGAGCACCCTGTGCGGTGGGGCAGAGGGCATCTGATGTGTGA 725
QY 861 agcctcagcagtcctccctcagcagaattccagtggtacaaagtacaaagactgtatga 920
Db 726 AGCCTCGCTGTGCCCTCTGTGACTTCCAGTGTACAAAGACAGACAGCGGCTGGCTGA 785
QY 921 aggaagaagaagggtgaaagtggaaacagaccttcctcctcaaaactcatcttctcaa 980
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QY 1041 caatgccagcatatgct 1058
Db 906 GCCGTCGCCCCACCATGCT 923

RESULT 8
AP004248/c 190864 bp DNA linear HTG 13-OCT-2001
LOCUS Homo sapiens chromosome 11 clone RP11-709M17 map 11q, WORKING DRAFT
DEFINITION
SEQUENCE, 14 unordered pieces.
ACCESSION AP004248
VERSION AP004248.1 GI:16117845
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-709M17.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 190864)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA of 11q
Published Only in Database (2001) in press
2 (bases 1 to 190864)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

TITLE
JOURNAL Submitted (12-OCT-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT
Genome Center
Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp

Project Information
Center project name: HumDrafl1
Center clone name: RP11-709M17

Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187825 bases at least Q40
Consensus quality: 188958 bases at least Q30
Consensus quality: 189416 bases at least Q20
Insert size: 189564; sum-of-contrigs
Quality coverage: 8.51x in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently consists of
14 contrigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contrigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

1 45963 contrig of 45963 bp in length
46064 73066 contrig of 27003 bp in length

73167 99513 contrig of 26347 bp in length
99614 117880 contrig of 18267 bp in length
117981 129001 contrig of 11021 bp in length
129102 137233 contrig of 8132 bp in length
137334 144978 contrig of 7645 bp in length
145079 152269 contrig of 7191 bp in length
152370 159751 contrig of 7382 bp in length
159852 167525 contrig of 7674 bp in length
167626 174628 contrig of 7003 bp in length
174729 182657 contrig of 7929 bp in length
182758 188251 contrig of 5494 bp in length
188352 190864 contrig of 2513 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 45963: contrig of 45963 bp in length
* 45964 46063: gap of 100 bp
* 46064 73066: contrig of 27003 bp in length
* 73067 73166: gap of 100 bp
* 73167 99513: contrig of 26347 bp in length
* 99514 99613: gap of 100 bp
* 99614 117880: contrig of 18267 bp in length
* 117881 117980: gap of 100 bp
* 117981 129001: contrig of 11021 bp in length
* 129002 129101: gap of 100 bp
* 129102 137233: contrig of 8132 bp in length
* 137234 137333: gap of 100 bp
* 137334 144978: contrig of 7645 bp in length
* 144979 145078: gap of 100 bp
* 145079 152269: contrig of 7191 bp in length
* 152270 152369: gap of 100 bp
* 152370 159751: contrig of 7382 bp in length
* 159752 159851: gap of 100 bp
* 159852 167525: contrig of 7674 bp in length
* 167526 167625: gap of 100 bp
* 167626 174628: contrig of 7003 bp in length
* 174629 174728: gap of 100 bp
* 174729 182657: contrig of 7929 bp in length
* 182658 182757: gap of 100 bp
* 182758 188251: contrig of 5494 bp in length
* 188252 188351: gap of 100 bp
* 188352 190864: contrig of 2513 bp in length.

FEATURES

Source

1.190864
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-709M17"
1.45963
/note="assembly_fragment"
46064..73066
/note="assembly_fragment"
73167..99513
/note="assembly_fragment"
99614..117880
/note="assembly_fragment"
117981..129001
/note="assembly_fragment"
129102..137233
/note="assembly_fragment clone_end:SP6 vector_side:right"
137334..144978
/note="assembly_fragment clone_end:T7 vector_side:left"
145079..152269
/note="assembly_fragment"
152370..159751
/note="assembly_fragment"
159852..167525

misc_feature /note="assembly_fragment"
167626.174628
misc_feature /note="assembly_fragment"
174729.182657
misc_feature /note="assembly_fragment"
182758.188251
misc_feature /note="assembly_fragment"
188352.190864
BASE COUNT 54344 a 40639 c 40476 g 54105 t 1300 others
ORIGIN

Query Match 36.6%; Score 619.8; DB 2; Length 190864;
Best Local Similarity 98.9%; Pred. No. 2.2e-146;
Matches 624; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1063 ggtccaggcgccgtcagcaggtgagcaacgagcagctcgaggaggcgagctgctg 1122
DB 74526 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGAGGGCAGGCTGCTGG 74467
QY 1123 ctgctgctctctgtgtcttgacacctcttcaaatlttgatgtgagtgccactlcccc 1182
DB 74466 CTGCTGCTCTTCTGTCTTGACCTGCTTCTCAAAATTTGATGTGAGTGCACCTTCCCC 74407
QY 1183 acccgaggaaagctgcccaccaccaccaccacacacagcaatgccaacccgacag 1242
DB 74406 ACCCGGAAAGGCTGCCGCCACCACCACACACAGCAATGGCAACCCGACAG 74347
QY 1243 caaccaatcagatatatacaaatgaattagaagaacaacacagctcctcagtgacagaat 1302
DB 74346 CAACCAATCAGATATATACAAATGAAATTGAGAGAAACACAGCCTCATGGGACAGAAATT 74287
QY 1303 tgaaggaggaggaaacaagaactttggygggaaaaaagtttaaaaaagaatltga 1362
DB 74286 TGAGGGAGGGGAACAAGAATACTTTGGGGGAAAGTTTAAAGAAATTGAAAA 74227
QY 1363 ttgcttgagatatattagtlacaatgagtttctttcccaacggygaagaacacagc 1422
DB 74226 TTGCTTGCAGATATATTAGGTACAAATGAGATTCTTTCCCAACGGGAAGACACAGC 74167
QY 1423 aacccggttggaaccaactgcaagctgcatctgtgaacctcttgggtgccaagtgggc 1482
DB 74166 AACCCGGCTTGGAACCCACTGCAAGCTGCATCGTGAACCTCTTGGTGGCAGTGTGGGC 74107
QY 1483 aagggtcagcctctctgcccacagagtgccccacgttggaacattctgagcttggccat 1542
DB 74106 AAGGGCTCAGCCTCTCTGCCCCACAGAGTGGCCCCACCTGGGAACATTCGTGAGCTGGCCAT 74047
QY 1543 cccaatcaatcagtcacatagagacgaacagaatagaacctccggcccaagcgtggcg 1602
DB 74046 CCCAAATTCATTCAGTCCATAGAGACGAACAGATGACCTTCCCGGCCCAAGCGTGGCG 73987
QY 1603 ctgcgaggcacttggtagactgtgcccacacgycgtgtgtgtgtaaacgtgaataaaaa 1662
DB 73986 CTGCGGGCAGCTTGGTAGACTGTGCCACACGCGGTGTGTGTAACGTTGAATTAATAAAA 73927
QY 1663 gagcaaaaaaaaaaaaaaaaaaaaaa 1693
DB 73926 GAGCAAGAAAGAAAAAGCAAAATTAAGA 73896

RESULT 9
AP000912/c 202505 bp DNA linear HTG 30-MAY-2000
LOCUS
DEFINITION Homo sapiens chromosome 11 clone RP11-715K6 map 11q25, WORKING
DRAFT SEQUENCE, 28 unordered pieces.
ACCESSION AP000912
VERSION AP000912.2 GI:8119054
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-715K6.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 202505)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 202,505 genomic DNA of 11q25
Published Only in Database (1999) In press
2 (bases 1 to 202505)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gs.riken.go.jp),
URL:http://hgp.gs.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997729.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gs.riken.go.jp/
Contact: hattori@gs.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-715K6
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 183541 bases at least Q40
Consensus quality: 192478 bases at least Q30
Consensus quality: 196692 bases at least Q20
Insert size: 199805; sum-of-contigs
Quality coverage: 4.09x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
28 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

1	26097	contig of	26097	bp	in	length
26198	48570	contig of	22373	bp	in	length
48671	65250	contig of	16580	bp	in	length
65351	78415	contig of	13065	bp	in	length
78516	91388	contig of	12873	bp	in	length
91489	102970	contig of	11482	bp	in	length
103071	112373	contig of	9303	bp	in	length
112474	123106	contig of	10633	bp	in	length
123207	133003	contig of	9797	bp	in	length
133104	142050	contig of	8947	bp	in	length
142151	150046	contig of	7896	bp	in	length
150147	156216	contig of	6070	bp	in	length
156317	161217	contig of	4901	bp	in	length
161318	166676	contig of	5359	bp	in	length
166777	171521	contig of	4745	bp	in	length
171622	175750	contig of	4129	bp	in	length
175851	178697	contig of	2847	bp	in	length
178798	183879	contig of	5082	bp	in	length
183980	186686	contig of	2707	bp	in	length
186787	188509	contig of	1723	bp	in	length
188610	191328	contig of	2719	bp	in	length
191429	193900	contig of	2472	bp	in	length
194001	195695	contig of	1695	bp	in	length
195796	197675	contig of	1880	bp	in	length
197776	198652	contig of	877	bp	in	length
198753	199845	contig of	1093	bp	in	length
199946	200982	contig of	1037	bp	in	length
201083	202505	contig of	1423	bp	in	length

Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	26097: contig of 26097 bp in length
26098	26197: gap of 100 bp
26198	48570: contig of 22373 bp in length
48571	48670: gap of 100 bp
48671	65250: contig of 16580 bp in length
65251	65350: gap of 100 bp
65351	78415: contig of 13065 bp in length
78416	78515: gap of 100 bp
78516	91388: contig of 12873 bp in length
91389	91488: gap of 100 bp
91489	102970: contig of 11482 bp in length
102971	103070: gap of 100 bp
103071	112373: contig of 9303 bp in length
112374	112374: gap of 100 bp
112474	123106: contig of 10633 bp in length
123107	123206: gap of 100 bp
123207	133003: contig of 9797 bp in length
133004	133103: gap of 100 bp
133104	142050: contig of 8947 bp in length
142051	142150: gap of 100 bp
142151	150046: contig of 7896 bp in length
150047	150146: gap of 100 bp
150147	156216: contig of 6070 bp in length
156217	156316: gap of 100 bp
156317	161217: contig of 4901 bp in length
161218	161317: gap of 100 bp
161318	166676: contig of 5359 bp in length
166677	166776: gap of 100 bp
166777	171521: contig of 4745 bp in length
171522	171621: gap of 100 bp
171622	175750: contig of 4129 bp in length
175751	175850: gap of 100 bp
175851	178697: contig of 2847 bp in length
178698	178797: gap of 100 bp
178798	183879: contig of 5082 bp in length
183880	183979: gap of 100 bp
183880	186686: contig of 2707 bp in length
186687	186786: gap of 100 bp
186787	188509: contig of 1723 bp in length
188510	188609: gap of 100 bp
188610	191328: contig of 2719 bp in length
191329	191428: gap of 100 bp
191429	193900: contig of 2472 bp in length
193901	194000: gap of 100 bp
194001	195695: contig of 1695 bp in length
195696	195795: gap of 100 bp
195796	197675: contig of 1880 bp in length
197676	197775: gap of 100 bp
197776	198652: contig of 877 bp in length
198653	198752: gap of 100 bp
198753	199845: contig of 1093 bp in length
199846	199945: gap of 100 bp
200982	contig of 1037 bp in length
200983	201082: gap of 100 bp
201083	202505: contig of 1423 bp in length.

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FEATURES
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      1. .202505
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="11"
        /map="11q25"
        /clone="RP11-715K6"
      1. .26097
        /note="assembly_fragment"
      26198. .48570
        /note="assembly_fragment"
      48671. .65250

```

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misc_feature /note="assembly_fragment"  
65351. .78415  
misc_feature /note="assembly_fragment"  
78516. .91388  
misc_feature /note="assembly_fragment"  
91489. .102970  
misc_feature /note="assembly_fragment"  
103071. .112373  
misc_feature /note="assembly_fragment"  
112474. .123106  
misc_feature /note="assembly_fragment"  
123207. .133003  
misc_feature /note="assembly_fragment"  
133104. .142050  
misc_feature /note="assembly_fragment"  
142151. .150046  
misc_feature /note="assembly_fragment"  
150147. .156216  
misc_feature /note="assembly_fragment"  
156317. .161217  
misc_feature /note="assembly_fragment"  
161318. .166676  
misc_feature /note="assembly_fragment clone_end:SP6 vector_side:left"  
166777. .171521  
misc_feature /note="assembly_fragment"  
171622. .175750  
misc_feature /note="assembly_fragment"  
175851. .178697  
misc_feature /note="assembly_fragment"  
178798. .183879  
misc_feature /note="assembly_fragment"  
183980. .186686  
misc_feature /note="assembly_fragment"  
186787. .188509  
misc_feature /note="assembly_fragment"  
188610. .191328  
misc_feature /note="assembly_fragment"  
191429. .193900  
misc_feature /note="assembly_fragment"  
194001. .195695  
misc_feature /note="assembly_fragment"  
195796. .197675  
misc_feature /note="assembly_fragment"  
197776. .198652
```

Query Match	36.5%;	Score 618.2;	DB 2;	Length 202505;
Best Local Similarity	98.7%;	Pred. No. 5,7e-146;		
Matches 623;	Conservative	0;	Mismatches 8;	Indels 0;
				Gaps 0;
QY 1063	gtgccaggcgccgctcagcgaggtgagcaacgycagctcgagggagggcgtgctctgg	1122		
Db 143589	GGTCCAGGCGCCGCTCAGCGAGGTGAGCAACGGCACCTCGAGAGGGCAGGCTGCGTCTGG	143530		
QY 1123	ctgctgcctcttctgctgttcttgcaactgcttctcgaatttggatgtgagtgccacttccc	1182		
Db 143529	CTGCTGCCTCTTCTGTGTCTTGACCTGCTCTCTCAATTTTGATGTGAGTGCACACTTCCC	143470		
QY 1183	accgggaaaggtctgctgcgcccacccacccacacacacagcaatgycaacaccgagag	1242		
Db 143469	ACCGGGAAAGGCTGCGCCACCAACCACCAACAACAGCAATGSCAACACCCGACAG	143410		
QY 1243	caaccaatcagatatataataaatagaataaagaacacagcctcatggyacagaaatt	1302		
Db 143409	CAACCAATCAGATATATACAAATGAATTAGAAGAACACAGCCTCATGGACAGAAATT	143350		
QY 1303	tgaaggaggggaaacaagaatactttggygggaaanaaagtttaaaaaaagaatgaaa	1362		
Db 143349	TGAGGAGGGGAACAAGAAATACTTTGGGGGGAAGAAAGCTTTTAAAAAAGAAATTGAAA	143290		
QY 1363	ttgccttgcatatatatagttacatgaggtttctctttcccaacggygaagacacagc	1422		
Db 143289	TTGCCTTCAGATATTTAGGTACCAATGGAGTTTCTTTCCCAACGGGAAAGAACACAGC	143230		

[illegible]

RESULT	12			
AP000832				
LOCUS	AP000832	187203 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 11 clone RP11-803P2 map 11q24, WORKING DRAFT SEQUENCE, 27 unordered pieces.			
ACCESSION	AP000832			
VERSION	AP000832.2	GI:8118984		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE	Homo sapiens DNA, clone:RP11-803P2.			

REFERENCE	1 (bases 1 to 187203)
AUTHORS	Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Toloki, Y., Watanabe, H. and Sakaki, Y.
TITLE	Human sapiens 187,203 genomic DNA of 11q24
JOURNAL	Published Only in Database (1999) In press
REFERENCE	2 (bases 1 to 187203)
AUTHORS	Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Toloki, Y., Watanabe, H. and Sakaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (03-DEC-1999) Masahira Hattori, The Institute of Physical

COMMENT On May 31, 2000 this sequence version replaced gi:56997666.

Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: <http://hgp.gsc.riken.go.jp/>
Contact: hattori@gsc.riken.go.jp
----- Project Information -----
Center project name: HumDraft11
Center clone name: RP11-803P2
----- Summary Statistics -----
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 171133 bases at least Q40
Consensus quality: 178533 bases at least Q30
Consensus quality: 182303 bases at least Q20
Insert size: 184603; sum-of-contigs
Quality coverage: 4.41x in Q20 bases; sum-of-contigs

27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1	30966	Contig of	30966	bp	in	length
31067	54248	Contig of	23182	bp	in	length
54349	68175	Contig of	13827	bp	in	length
68276	78752	Contig of	10477	bp	in	length
78853	88975	Contig of	10123	bp	in	length
89076	98751	Contig of	9676	bp	in	length
98852	107804	Contig of	8953	bp	in	length
107905	116364	Contig of	8460	bp	in	length
116465	125558	Contig of	9094	bp	in	length
125659	130702	Contig of	5044	bp	in	length
130803	135910	Contig of	5108	bp	in	length
136011	142273	Contig of	6263	bp	in	length
142374	149281	Contig of	6908	bp	in	length
149382	155493	Contig of	6112	bp	in	length
155594	161282	Contig of	5689	bp	in	length
161383	165649	Contig of	4267	bp	in	length
165750	169554	Contig of	3805	bp	in	length
169655	170397	Contig of	743	bp	in	length
170498	173675	Contig of	3178	bp	in	length
173776	175501	Contig of	1726	bp	in	length
175602	177711	Contig of	2110	bp	in	length
177812	180070	Contig of	2259	bp	in	length
180171	182293	Contig of	2123	bp	in	length
182394	183405	Contig of	1012	bp	in	length
183506	184693	Contig of	1188	bp	in	length
184794	186078	Contig of	1285	bp	in	length
186179	187203	Contig of	1025	bp	in	length
Sequence updated (26-May-2000).						

```
* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

*	1	30966: contig of 30966 bp in length
*	30967	31066: gap of 100 bp
*	31067	54248: contig of 23182 bp in length
*	54249	54348: gap of 100 bp
*	54349	68175: contig of 13827 bp in length
*	68176	68275: gap of 100 bp
*	68276	78752: contig of 10477 bp in length
*	78753	78852: gap of 100 bp
*	78853	88975: contig of 10123 bp in length
*	88976	89075: gap of 100 bp
*	89076	98751: contig of 9676 bp in length
*	98752	98851: gap of 100 bp
*	98852	107804: contig of 8953 bp in length
*	107805	107904: gap of 100 bp
*	107905	116364: contig of 8460 bp in length
*	116365	116464: gap of 100 bp
*	116465	125558: contig of 9094 bp in length
*	125559	125658: gap of 100 bp
*	125659	130702: contig of 5044 bp in length
*	130703	130802: gap of 100 bp
*	130803	135910: contig of 5108 bp in length
*	135911	136010: gap of 100 bp
*	136011	142273: contig of 6263 bp in length
*	142274	142373: gap of 100 bp
*	142374	149281: contig of 6908 bp in length
*	149282	149381: gap of 100 bp
*	149382	155493: contig of 6112 bp in length
*	155494	155593: gap of 100 bp
*	155594	161282: contig of 5669 bp in length
*	161283	161382: gap of 100 bp
*	161383	165649: contig of 4267 bp in length

University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK

FEATURES

URES	Location/Qualifiers
source	1. .1556
	/organism="Gallus gallus"
	/db_xref="taxon:9031"
	/tissue_type="brain"
	/dev_stage="E18"
gene	1. .1556
	/gene="OBCAM"
CDS	17. .1051

BASE COUNT	305 a	481 c	477 g	293 t
ORIGIN				

Query Match	32.6%;	Score 551.8;	DB 5;	Length 1556;
Best Local Similarity	73.3%;	Pred. No. 1.8e-129;		
Matches 706;	Conservative	0;	Mismatches 257;	Indels 0;
				Gaps 0;

QY	210	aggagtgccctgtgcgacgcggagatgccaacctcccccaagaattgacaacgltgacggt	269
Dd	97	AGGAGTGCCCGTGC CGACGGAGATGCCACCCTTCCCCAAAGCTATGGACAACGTGACTGT	156
QY	270	ccggcaaggggagagcgccaacctcagttgacatttgaacaaccggtcacccgggtgac	329
Dd	157	GCGGCAAGGGGAGAGTCCCACGCTCAGGTGTACCGGTGATGACAGGGGTGAGCGGGTAC	216
QY	330	ctggtcaaacccgcaaccatccttatgtcgtggaaatgacaagtgtgcctgatccctcg	389
Dd	217	GTGGTTGAACCGCACGACCATCTTTATGCTGGCAATGACAGTGGTCTATTAGACAACCG	276
QY	390	cgtgtcctctctgagcaacaaccaacycagtacagcatcgagatcccagaactgtgatt	449
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LOCUS	BTOBCAM
DEFINITION	Bovine mRNA for opioid binding protein/cell adhesion molecule
ACCESSION	X12672
VERSION	X12672.1
KEYWORDS	GI:585 cell adhesion molecule; glycoprotein; immunoglobulin superfamily; membrane protein; opioid binding protein.
SOURCE	COW.
ORGANISM	Bos taurus
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MEDLINE	
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Query Match

32.28; Score 545.4; DB 4; Length 2593;

Best Local Similarity 73.6%; Pred. No. 8.6e-128;

Matches 709; Conservative 0; Mismatches 251; Indels 3; Gaps 1;

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Db	925	CCGCGAGGGGAGAGGCCACCCTCAGATGTACCATAGATGATCGGGTCACCCGGGTGGC	984
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GenCore version 4.5
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Title: US-09-700-397-1

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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 7, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414, 657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...924
; OTHER INFORMATION:
; US-08-414-657D-7

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Best Local Similarity 63.3%; Pred. No. 1.2e-93;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

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; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat

APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 2..976
OTHER INFORMATION:
US-08-414-657D-1

Query Match 33.0%; Score 340.6; DB 2; Length 977;
Best Local Similarity 63.3%; Pred. No. 1.2e-93;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 72 tctctccaagagatgcccgtgacgagatgcccaccttccccaaagtattgacaa 131
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QY 1032 t 1032
Db 1014 T 1014

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; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
US-08-414-657D-3

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Query Match 33.0%; Score 340.6; DB 2; Length 1238;
 Best Local Similarity 61.9%; Pred. No. 1.3e-93;
 Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

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QY 72 tctctcgaagagtgcccgctgcgacgagagatgccaacctccccaaagtatggaaca 131
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Db 121 TCTTCCACAGGACTGCCGCTTCGACAGGTGAT-----TTAACCGAGGACAGCAAA 174

QY 132 cgtgacggtccgacgagagagagcgccacctcaagtgactatgaacacgggtcac 191
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Db 175 CATCACCGTGAAGCAGGAGGACACGAGCCATCTCAGGTGTGTGTGTAAGACAAGAACTC 234

QY 192 ccggtgtgctgtgtaaacgcagcaacctctatgtgtggaatgacaagtgtgacct 251
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Db 235 GAAAGTGCCCGTTGAGACCGCTCTGGCAATCATCTTCGCTGGACACAGCAAGTGGTCT 294

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Db 295 GAACCCCTCGGATTGAGCTGAGAAACCGCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

QY 312 cgtgagtgtatgacgagggcccttacacctgtcgtgtgcagacagacaaccaccaaa 371
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Db 355 GGTGGATGTCTATGATGAAGGATCTTACACATGCTCAGTTTCAGACACAGCATGAGCCCAA 414

QY 372 gaacctagagttccacctatgtgcaaglatctcccaaatgttagagattctcaga 431
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Db 415 GACCTCTCAAGTTTACTTGATGTATGATTCACCAAGTTCACCAAGATCCCAACATCTCTCGGA 474

QY 432 tatctccatlaatgaaggaacaatatatgacctacacctgcatagcaactgtagaccaga 491
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Db 475 TGTCACTGTGATGAGGCGCAATGTACCTGTGTCCATGTGGCAATGGCGCCCTGA 534

QY 492 gacctagtgtaacttgagagacacatctctcccaagcggtgtgtgtgtgtgtgtgtgt 551
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Db 535 ACCTGTATACCTTGAGAGACACTTACACCACTTGAGAGAGATTTGAAGAGAGAAGA 594

QY 552 atacttgaattcagggcaccaccccgagcagtcagtgagtgactagtgagtgctc 611
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Db 595 ATATCTGAGATCTTAGGACATCACAGGGAACAGTCAGGCCAATATATGATGCAAGGCTGC 654

QY 612 caatgacgtgcgcgcgcgtgtgtacgagagtaaggtcacctgataccaccata 671
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Db 655 CAACGAGGTCTCTCCGCGGATGTCAAAAGTCAAGGTCACTGTGAATATTCACCCAC 714

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Db 775 AGCCTCAGCGGTCCCTGACACTGACTTGAAGTGTACCGGATGACACACAG--GATAAA 831

QY 792 aggaagaaggggtgaagtggaacagacaccttctctcaaacatcatcttctcaa 851
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Db 832 CAGTGCACAGCGCCTTGAGATTAAAGACACTGAGGCCAGTCCCTGACGGTGAACCAA 891

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Db 892 CGTCACTGAGGACACTACGGCAACTATATCTGTGTGCTGCCAACAGCTCGGCGTAC 951

QY 912 caatgccagcatatgtattgtccagcgccgctcagcagagtgaagcaacgagcagtc 971
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QY 1032 t 1032
Db 1069 T 1069

RESULT 5
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283

```



```

1  GENERAL INFORMATION:
2  APPLICANT: Levitt, Pat
3  APPLICANT: Pimenta, Aurea
4  APPLICANT: Fischer, Itzhak
5  APPLICANT: Zhukareva, Victoria
6  TITLE OF INVENTION: Limbic System-Associated Membrane
7  TITLE OF INVENTION: Protein and DNA
8  NUMBER OF SEQUENCES: 60
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Dechert Price & Rhoads
11 STREET: 997 Lenox Drive, Building 3, Suite 210
12 CITY: Lawrenceville
13 STATE: NJ
14 COUNTRY: USA
15 ZIP: 08543
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FastSeq for Windows Version 2.0
22
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/414,657D
25 FILING DATE: 31-MAR-1995
26 CLASSIFICATION: 435
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER:
29 FILING DATE:
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Bloom, Allen
32 REGISTRATION NUMBER: 29,135
33 REFERENCE/DOCKET NUMBER: 317743-102
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 609-520-3214
36 TELEFAX: 609-520-3259
37
38 TELEX:
39
40 INFORMATION FOR SEQ ID NO: 9:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 861 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: double
45 TOPOLOGY: linear
46
47 FEATURE:
48 NAME/KEY: Coding Sequence
49 LOCATION: 1..861
50 OTHER INFORMATION:
51
52 US-08-414-657D-9

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Query Match	32.8%;	Score 338.6;	DB 2;	Length 861;
Best Local Similarity	63.7%;	Pred. No. 4.5e-93;		
Matches 531;	Conservative	0;	Mismatches 299;	Indels 3;
				Gaps 1;
QY 120	agctatgacaacgctgtgaacgctccgcgcgaggggagagcgccaccctcaggtgcactatga	179		
Db 24	AGGCACGGACACACATCACCGGTGAGGCGAGGGGACACAGCCATCCTCAGGTGCGTTCFAGA	83		
QY 180	caaccggttcacccggtgtgccttgctgttaaacgcgcagcaccatcctctatgcttggnaatga	239		
Db 84	AGACACAGACTCAAAGGTGGCCCTGGTTGAACCGTTCTGGCATCATTTTTCCTGGACATGA	143		
QY 240	caagtgctgcttgatctctgcgctgtgctctcttgagcaacacccaacgcaagtacagcat	299		
Db 144	CAAGTGTCTCTGGACCCACCGGTTGAGCTTGAGAAAGCCATCTCTCGAATACAGCCT	203		
QY 300	cgagatccagaacgctgcatgtgtatgacgagggcccttacacctgtctcggtgcagacaga	359		
Db 204	CCGAATCCAGAAGGTGATGTCTATGATGAGGGTTCTTACACTTGCCTCAGTTCCAGACACA	263		
QY 360	caaccaccccaagacctctaggtgccacctcaattgtgcaagtatatctccaaaattgttga	419		
Db 264	GCAATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAGTCCCCACCAAGAAGTCTCCAA	323		
QY 420	gatttctcagatatcttcattaatatgaagggaacaatatattagcctcaactgcatagcaac	479		

Db	324	TATCTCTCTGGGATGTCACTGTGATGAGG66CAGCAACGTGACTCTGTGTGATGGCCAA	383
QY	480	tgtgtagccagagcctacggttacttggagacacatctctcccaagcglttggcttgt	539
Db	384	TGGCCGTCTCTGAACCTGTTATTCACCTGGAGACACCTTACACCAACTGGAAGGAATTGA	443
QY	540	gagtgaagacgaatacttggaaattcagggcatcacccggagcagtcagggactacga	599
Db	444	AGGAGAAGAAGAATATCTGGAGATCTTGGCATCACCAGGAGAGCACTCAGGCAAAATATGA	503
QY	600	gtgcagtgccctccaatgacgtygcgcgcgcgcgtgtgtacgagagttaaaagtccacgtgaa	659
Db	504	GTGCAAGAGCTGCCAACAGAGGCTCTCCCTGGCGGATGTCAAACAAGTCAAGTCACTGTGAA	563
QY	660	ctatccaccatacatcttcagaagccaaggygtacaggtgtcccgtyggyacaaaggygac	719
Db	564	CTATCTCTCCACACTATCACAGATCCCAAGSCAATGAAGCCACCAAGACGACACAAGCTTC	623
QY	720	actgcagtggtgaagcctcagcagctcccttcagcagaattccagttygtacaaagatgacaa	779
Db	624	ACTCAATAGTGAGGCGCTCGGAGAGTGCCTGCACACTGACTTTGAGTGTATACCGGAGTGCAC	683
QY	780	aagactgattggaaggaagaaggygtgaaagtgtgaaaaacagaccttccctccaact	839
Db	684	TAG---GATAAATAGTGCCCATGGCCCTTTAGATTAGAGACGACGGGCGGCTTTCCCT	740
QY	840	catcttcttcaatgtctctgtaacatgactatyggaactatacaacttgcgttgccctcaacaa	899
Db	741	GACGGTGACCAACGCTCACTGAGGAGCACAATTACGGCAACTACACCTGTGTGGCTGCCAACAA	800
QY	900	gctgggccaacccaatgccaagcatcatgtatttgttccaggcgccggtcagcg	952
Db	801	GCTGGGGGTCAACCAATGCCAGCGCTAGTCCCTTTTCAGACCTGGGTGGGTGAGAG	853

RESULT 6
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214


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Db      240 GGACCCTCGGGTTGAGCTGGAGAAACGCCCATGCTCTGGAAATACAGCCCTCCGAATCCAGAA 299
QY      312 cgtgatgtgtatgaacagagggcccttaacactgtctggtgcagacagacaaccaccaa 371
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Db      300 GGTGATGTCTATGATGAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCAA 359
QY      372 gacctagggtccaccctcatgtgtcaagtatctccaaatgttagagatttctcaga 431
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      360 GACCTCTCAAGTTTACTTGATTTGACAGTTCACCAAAGATCTCCACATCTCTCGGA 419
QY      432 tatctccalttaatgaagggaacatatatagcctcactgtcatagcaactgtgtgaccaga 491
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Db      420 TGTCACTGTGAATGAGGGCAGCAATGTAAACCTGGTCTGCATGGCCATGGGCCCTTGA 479
QY      492 gcttaacgttaacttggagaacacatctctcccaagcggttgcttltgtgagtaagaca 551
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Db      480 ACCTGTTATCACTGGAGACACCTTACACCACCTTGGAAAGAGAAITTTGAAGGAGAAAGA 539
QY      552 ataacttggaaattcaagggcatcacccggagcgactcagggactacgagtgcgtc 611
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        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      660 CATTCACAGAGTCTAAGACCAATGAAGCCACACAGGACGACAGCACTTCCCTCAATGTGA 719
QY      732 agccctcagcagtcctccctcagcagaatctcagttgtgtacaagatgacaaaagactgtatga 791
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Db      720 AGCCTCAGCGGTGCTCCCTGCACCTGACTTTGAGTGTGATCCGGATGACACCAG--GATAAA 776
QY      792 aggaagaaggggtgtgaaagltgaaaaacagaccttctctcaaaactcatcttctcaa 851
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Db      777 CAGTGCAACGCGCCTTGAGATTAAGAGCACTGAGGGCCAGTCTCTCCCTGACGGTGACCA 836
QY      852 tgtctctgaacatgactatggaaactaacacttgcgtggtcctcaacaagctgggccacac 911
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Db      837 CGTCACTGAGGAACACTACGCGCAACTATACCTGTGTGGCTGCCAACAAGCTCGCGCTCAC 896
QY      912 caatgcagcatcatgtcatattgtgtccagggcgctcagcg 952
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Db      897 CAATGCCAGCCTAGTCTTTTCAGACCCGGGTGGTAGAG 937

RESULT      8
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
;

```

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; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 10:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
;
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
;
US-08-414-657D-10

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Query Match	32.3%	Score 333.8;	DB 2;	Length 861;
Best Local Similarity	63.4%;	Pred. No. 1.3e-91;		
Matches 528;	Conservative	0;	Mismatches 302;	Indels 3;
				Gaps 1;
QY 120	agctatgacacacgctgacggtccgcgcaggggagagcgccaccctcaggtgcactattga	179		
DB 24	AGGCACGGACACACATCACCGGTGAGGCGAGGGGACACGGCCATCCCTCAGGTGTGTGTAGA	83		
QY 180	caaccgggtcacccgggtgycctgctaaaccgcacacatcctctatgctgysaatga	239		
DB 84	AGACACAGAACTCGAAGAGTGCGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGA	143		
QY 240	caagtgggtcctgcatcctcgcgctggtcctctctgagcaacacccaaacgcagtlacagcat	299		
DB 144	CAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCT	203		
QY 300	cgcagatccagaacgctgcatgtgtatgacagagcgccctlacacctgctcgtgpcagacaga	359		
DB 204	CCGATCCAGAAAGGTGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCCAGACACA	263		
QY 360	caaccaccnaagacctagagttccacctatgtgcaagtatctcccaaatctgata	419		
DB 264	GCATGAGCCCAAGACCTCTCAAGTTTACTGTGATGTACAGTTCCACCAAGATCTCCAA	323		
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DB 444	AGGAGAAAGAAATATCTGGAGATCCTAGGCATCACCGGAACAGTCACGCAATATGA	503		
QY 600	gtgcagtgccctccaatgacgtgycgcgcgcctggtacgagagtaaatggtcacccgtga	659		
DB 504	GTCGAGAGGCTGCCACAGAGAGGTCTTCCTCCGGGATGTCAACAAGTCAAGTCTGTGAA	563		
QY 660	ctatccaccataacttcagaagccaaggttacaggtgtcccccgtgggacaaaaggggac	719		
DB 564	CTATCCACCCACCATCATCAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAGCTTC	623		
QY 720	actgcagtgtagaagcctcagcagtcocctcagcagaattccaggtgtlacaaagatgacaa	779		
DB 624	CTTCAAAATGTGAGGCTCAGCGGTGCTGCACCTGACTTTGAGTGGTACCGGGGTGACAC	683		

QY 780 aagactgattgaaggaaggggtgaagtggaacacagaccttctcctcaaac 839
Db 684 CAG---GATAAACAGTGCACAAACGGCCCTGAGATTAAAGACACTGAGGGCCAGTCCCT 740
QY 840 catctcttcaatgtctgaacatgactatggaactacacttgctggcctcaaca 899
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RESULT 9

US-08-414-657D-17

; Sequence 17, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

; APPLICANT: Levitt, Pat

; APPLICANT: Pimenta, Aurea

; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane

; TITLE OF INVENTION: Protein and DNA

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/414,657D

; FILING DATE: 31-MAR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bloom, Allen

; REGISTRATION NUMBER: 29,135

; REFERENCE/DOCKET NUMBER: 317743-102

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-520-3214

; TELEFAX: 609-520-3259

; TELEX:

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 756 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1..756

; OTHER INFORMATION:

; US-08-414-657D-17

Query Match

Best Local Similarity 29.4%; Score 303.6; DB 2; Length 756;

Matches 481; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 148 ggggagagcgccacccctcaggtgactattgacaaccgggtcaccgggtggctgcta 207
Db 1 GGGGACACAGCCATCTCAGGTGCTTCTAGAGACACAGAACTCAAAAGGTGGCTGTG 60

QY 208 aaccgcagcaccatcctctatgtctggtgaatgacaagtgtgctcgtgatcctcgtgtgc 267
Db 61 AACCGTCTGGCATCATTTTTTCTGGACATGACAACTGCTCTCTGACCCACGGGTGAG 120
QY 268 ctctgagcaacaccccaaacgcagctacagcatcgagatccagaacgttgatgtatgac 327
Db 121 CTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAGGTGATGCTATGAT 180
QY 328 gaggcccttacacctgctcgtgagacagacacaccccaaacctctaggtccac 387
Db 181 GAGGTTCTTACACTTGTCTCAGTTTCAGACACACAGCATGAGCCCAAGACCTCCCAAGTTTAC 240
QY 388 ctcatgtgcaagtatctcccaaatgtagagattctcagatatctccatlaatgaa 447
Db 241 TTGATCGTACAGTCCCAACCAAGATCTCCAATATCTCCTCGGATGTCACCTGGAATGAG 300
QY 448 gggacaatatagcctcaccctgcatagcaactgtagaccagaagcctacggttacttg 507
Db 301 GGCAGCAACGTGACCTCTGCTGCTGCAATGGCCCAATGGCCGCTCTGAACCTGTATCACCTGG 360
QY 508 agacacatctctcccaaacgcggttgcttgtgtgagtgaagacgaatcttggaattcag 567
Db 361 AGACACCTTTACACCACTGGAAGGAATTTGAAGGAGAGAGAGAAATATCTTGAGATCTCTT 420
QY 568 ggcatacccgaggagcagtcaggggactacgagtgcagtgcctccaatgacgtgcccgc 627
Db 421 GGCAATCACCAAGGAGCAGTCAGGCAATATGAGTGAAGCTGCCCCAACGAGGTCTCTCG 480
QY 628 cccgtgtacgagagtaaaagtcaacgtgactatccacatattcagaagccaag 687
Db 481 GCGATGTCAAAACAAGTCAAGGTCACTGTGAATATCTCCCACTATCACAGAAATCCAAG 540
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Db 541 AGCAATGAAGCCACACAGCAGCAGCAAGCTTCACTCAATGTGAGGCCCTCGGACAGTGCTT 600
QY 748 tcagcagaattccaggtgtacaaagtacaaaagactgattgaagaaagaaaggggtg 807
Db 601 GCACCTGACTTTGAGTGTGATCCGGGATGACACTAG--GATAAATAGTGCCAATGGCCTT 657
QY 808 aaagtggaaaacagaccttctctcacaactcatctcttcaatgtctctgaacatgac 867
Db 658 GAGATTAAAGACAGCAGGAGGCGCATCTTCCCTGACGCGTGACCAACGTCATGAGGAGCAC 717
QY 868 tatgygaactacacttgctggtcctccaacaagctggg 905
Db 718 TACGGCAACTACACTGTGTGGCTGCCAACCAAGCTGGG 755

RESULT 10

US-08-414-657D-18

; Sequence 18, Application US/08414657D

; Patent No. 5861283

; GENERAL INFORMATION:

; APPLICANT: Levitt, Pat

; APPLICANT: Pimenta, Aurea

; APPLICANT: Fischer, Itzhak

; APPLICANT: Zhukareva, Victoria

; TITLE OF INVENTION: Limbic System-Associated Membrane

; TITLE OF INVENTION: Protein and DNA

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS


```
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..756
OTHER INFORMATION:
US-08-414-657D-18

Query Match      28.9%; Score 298.2; DB 2; Length 756;
Best Local Similarity 63.0%; Pred. No. 7.5e-81;
Matches 478; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

QY 148 ggggagagcgccaccctcagtgctcctattgacacccggtgaccccggtgctgcta 207
Db 1 GGGGACACGGCCATCCTCAGGTGCTGTAGAGACCAAGAACTCGAAAGTGGCCTGTTG 60
QY 208 aaccgacgacccatcctctatgctggaatgacaaagtgtgctgctgctgctgctg 267
Db 61 AACCGCTCTGGCATCTCTGCTGGACACGACAGAGTGTCTGTGACCCCTGGGTTGAG 120
QY 268 ctctgagcaacaccccaaacgagctacagcatcgatccagaaagtgtgctgctgac 327
Db 121 CTGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAAGTGTGATCTATGAT 180
QY 328 gaggcccttacacctgctcggtgacagacacacaccccaaacacccctctaggtccac 387
Db 181 GAAGGATTCCTACACATGCTCAGATCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTAC 240
QY 388 ctcatgtgcaagtatctcccaaaattgtagaattctctcagatatctccattaatgaa 447
Db 241 TTGATGTACAGATTCACCAAAAGATCTCCAACATCTCCTCGATGTCTGATGATGAG 300
QY 448 gggacaataatagcctcaccctgacactgtagaaccagagcctacgcttactgtg 507
Db 301 GGCAGCAATGTAACCTGTGCTGTGATGGCCATGGCGCCCTGAACCTGTATACCTTG 360
QY 508 agacacatctctcccaaacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 567
Db 361 AGACACCTTACACCACTTGAAGAAGATTGGAAGAGAGAAGAAATATCTGGAGATCTTA 420
QY 568 ggcatacccggtgagcagctgagcagctgagcagctgagcagctgagcagctgagcag 627
Db 421 GGCATCACCGGAGAGAGTCAAGCAAAATATGATGCAAGGCTGCCAAGAGCTCTCTCC 480
QY 628 cccgtggtacgagagtaaggtacacctgaactatccaccatacatttaagaagccaag 687
Db 481 GCGATGTCAACAAAGTCAAGGTCACTGTGAATATCCACCCACCATCAGAGAGTCTTAAG 540
QY 688 ggtacaggtgtcccgctggtgacaaaagggagacactgcaagtgtgaagcctcagcagtc 747
Db 541 AGCAATGAAGCCACACAGGACGACCAAGCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCT 600
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QY 748 tcagcagaattccagtggtacaaagatgacaaaagactgattgaaagaaaggggtg 807
Db 601 GCACCTGACTTGTAGTGTGTACCGGATGACACCCAG--GATTAACAGTGCACACGGCCTT 657
QY 808 aaagtggaaaacagaccccttcctcctcaaaactatcttctcaatgtctctgaacatgac 867
Db 658 GAGATTAAAGACACTGAGGGCCAGTCTCCTCGACGCTGACCAACGTCACCTGAGGAACAC 717
QY 868 tatggaaactacacttgcgtgctcctcaacaaagtggc 906
Db 718 TACGGAACTATACCTGTGTGCTGTGCCAACAAAGCTCGGC 756
```

```
RESULT 11
US-08-414-657D-11
Sequence 11, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Dechart Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..219
OTHER INFORMATION:
US-08-414-657D-11
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```
Query Match      9.7%; Score 100; DB 2; Length 219;
Best Local Similarity 67.0%; Pred. No. 5.2e-21;
Matches 142; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 148 ggggagagcgccaccctcagtgctgacactatgacaaaccggtcaccgggtgctgcta 207
Db 1 GGGGACACAGCCATCTCAGGTGCGTCTAGAGAGACAACTCAAGAGTGGCCTGTTG 60
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[illegible]

RESULT 12
US-08-414-657D-12
; Sequence 12, Application US/08414657D
; Patent No. 5861283

```

: GENERAL INFORMATION:
: APPLICANT: Levitt, Pat
: APPLICANT: Pimenta, Aurea
: APPLICANT: Fischer, Itzhak
: APPLICANT: Zhukareva, Victoria
: TITLE OF INVENTION: Limbic System-Associated Membrane
: TITLE OF INVENTION: Protein and DNA
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESS: Dechert Price & Rhoads
: STREET: 997 Lenox Drive, Building 3, Suite 210
: CITY: Lawrenceville
: STATE: NJ
: COUNTRY: USA
: ZIP: 08543
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/414,657D
: FILING DATE: 31-MAR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bloom, Allen
: REGISTRATION NUMBER: 29,135
: REFERENCE/DOCKET NUMBER: 317743-102
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-520-3214
: TELEFAX: 609-520-3259
: TELEX:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 219 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1...219
: OTHER INFORMATION:
:
: US-08-414-657D-12

```

Query Match 9.2%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 1.5e-19;
Matches 139; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 148 ggggagagcgccaccctcaggtgcacattgacaaacggtcacccggtgtgcctgcta 207
||||| | ||||| ||||| | ||| | | ||||| |
Db 1 ggggacacggcccatctctcagctgtgttgtagaagacacagaacttcgaagctgccttggttg 60

QY	208	aaccgcagcaccatccctatgtctggaatgacaagtgtgccttgatacctcgctgttc	267
Db	61	AACCGCTCTGGCATCATCTTCGCTGCACACGACACAGTGTCTCTGGACCCTCGGTTGAG	120
QY	268	cttctagcaacacccccaaacgcagtlacagcatctgagatccagaacctgtatgttatgac	327
Db	121	CTGGAGAAGCCCATGCTCTTGGAATACAGCCTCCCAATCCAGAAAGGTGGATGTCTATGAT	180
QY	328	gaggggcccttacacctgtctcgltgcagacaga	359
Db	181	GAAAGATCCTAACACATGCTCAGTTACAGACA	212

RESULT 13
US-08-414-657D-13
; Sequence 13, Application us/08414657D
; Patent No. 5861283

```

: GENERAL INFORMATION:
: APPLICANT: Levitt, Pat
: APPLICANT: Pimenta, Aurea
: APPLICANT: Fischer, Itzhak
: APPLICANT: Zhukareva, Victoria
: TITLE OF INVENTION: Limbic System-Associated Membrane
: TITLE OF INVENTION: Protein and DNA
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dechert Price & Rhoads
: STREET: 997 Lenox Drive, Building 3, Suite 210
: CITY: Lawrenceville
: STATE: NJ
: COUNTRY: USA
: ZIP: 08543
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/414,657D
: FILING DATE: 31-MAR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bloom, Allen
: REGISTRATION NUMBER: 29,135
: REFERENCE/DOCKET NUMBER: 317743-102
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-520-3214
: TELEFAX: 609-520-3259
: TELEX:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 177 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1..177
: OTHER INFORMATION:
:
US-08-414-657D-13

```

Query Match	7.5%;	Score 77.8;	DB 2;	Length 177;
Best Local Similarity	65.0%;	Pred. No. 2.5e-14;		
Matches 115;	Conservative 0;	Mismatches 62;	Indels 0;	Gaps 0;

QY 448 ggaacacatatatgacctcacctgcataagcaactgtgtagaccagacctaacgtractctgg 507
||| ||| | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ggacagcAACCTGACTCTGTGCTGTGCATGGCCCAATGGCGTCCCTGAACCTGTATTACACCTGG 60

QY 886 gtggcctccacaagctggg 905
|||||
Db 178 GTGGCTGCCCAACAAGCTGGG 197

Search completed: July 11, 2002, 22:53:23
Job time: 13212 sec